

GenCore version 5.1.9
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OM protein - protein search, using SW model

Run on: July 12, 2006, 05:39:35 ; Search time 49 Seconds
(without alignments)
26.795 Million cell updates/sec

Title: US-10-671-019-2

Sequence: 1 VPFSAKSVKSLYLIG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 249102

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 800 summaries

Database :

Issued Patents AA:*

- 1: /EMC_Celerra_SIDS3/prodata/2/iaa/5 COMB.pep:*
- 2: /EMC_Celerra_SIDS3/prodata/2/iaa/6 COMB.pep:*
- 3: /EMC_Celerra_SIDS3/prodata/2/iaa/7 COMB.pep:*
- 4: /EMC_Celerra_SIDS3/prodata/2/iaa/8 COMB.pep:*
- 5: /EMC_Celerra_SIDS3/prodata/2/iaa/9 COMB.pep:*
- 6: /EMC_Celerra_SIDS3/prodata/2/iaa/10 COMB.pep:*
- 7: /EMC_Celerra_SIDS3/prodata/2/iaa/backfill1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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1	36	50.0	12	2	US-09-185-501B-6	Sequence 6, Appl1
2	27.5	38.2	14	2	US-09-305-781-2	Sequence 2, Appl1
3	27	37.5	9	3	US-09-641-528B-11725	Sequence 2131, Ap
4	27	37.5	9	3	US-09-641-528B-11725	Sequence 11725, A
5	27	37.5	9	3	US-09-641-528B-24500	Sequence 24500, A
6	27	37.5	10	3	US-09-641-528B-2132	Sequence 2132, Ap
7	27	37.5	10	3	US-09-641-528B-11726	Sequence 11726, A
8	27	37.5	10	3	US-09-641-528B-20365	Sequence 20365, A
9	27	37.5	10	3	US-09-641-528B-24501	Sequence 24501, A
10	27	37.5	11	3	US-09-641-528B-16759	Sequence 16759, A
11	27	37.5	11	3	US-09-641-528B-20366	Sequence 20366, A
12	27	37.5	11	3	US-09-641-528B-24535	Sequence 24535, A
13	27	37.5	11	3	US-09-641-528B-46330	Sequence 46330, A
14	27	37.5	12	1	US-08-457-528B-51190	Sequence 51190, A
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17	26	36.1	12	1	US-08-465-217A-34	Sequence 34, Appl1
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78	26	36.1	9	2	US-09-166-448-72	Sequence 72, Appl1
79	26	36.1	9	2	US-09-567-979-31	Sequence 31, Appl1
80	26	36.1	9	2	US-09-249-27-5	Sequence 5, Appl1
81	26	36.1				

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.308
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11703
FILING DATE: 28-DEC-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/984,852
FILING DATE: 02-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Green, Grant D.
REGISTRATION NUMBER: 31,259
REFERENCE/DOCKET NUMBER: 0222.101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2706
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-11703-54

Query Match 36.1%; Score 26; DB 5; Length 15;
Best Local Similarity 66.7%; Pred. No. 4.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 KSLYIG 15
DB 4 KSIYIG 9

RESULT 29
PCT-US93-11703-55
Sequence 55, Application PC/TUS9311703
GENERAL INFORMATION:
APPLICANT: Chiron Miotopes Pty. Ltd.
TITLE OF INVENTION: T-Cell Epitopes
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Grant D. Green
STREET: 4560 Horton St.
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.308
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11703
FILING DATE: 28-DEC-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/984,852
FILING DATE: 02-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Green, Grant D.
REGISTRATION NUMBER: 31,259
REFERENCE/DOCKET NUMBER: 0222.101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2706
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
PCT-US93-11703-55

Query Match 36.1%; Score 26; DB 5; Length 15;
Best Local Similarity 66.7%; Pred. No. 4.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 KSLYIG 15
DB 2 KSIYIG 7

RESULT 30
US-08-787-547-62
Sequence 62, Application US/08787547
Patent No. 578567
GENERAL INFORMATION:
APPLICANT: Hedley, Mary Lynne
APPLICANT: Curley, Joanne M.
APPLICANT: Langer, Robert S.
TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY
TITLE OF INVENTION: OF NUCLEIC ACID
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/787,547
FILING DATE: 22-JAN-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 08191/003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-787-547-62

Query Match 34.7%; Score 25; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPSV 5
DB 5 VPSV 9

RESULT 31
US-08-417-174-48
Sequence 48, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,

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APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & PINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-417-174-48

Query Match 34.7%; Score 25; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPFSV 5
DB 5 VPFSV 9

RESULT 32
US-08-417-174-83
Sequence 83, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & PINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-417-174-83

Query Match 34.7%; Score 25; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPFSV 5
DB 5 VPFSV 9

RESULT 33
US-08-417-174-84
Sequence 84, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & PINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:

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OM protein - protein search, using sw model

Run on: July 12, 2006, 05:39:35 ; Search time 49 Seconds
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26.795 Million cell updates/sec

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SUMMARIES

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3	27	37.5	9	3 US-09-641-528B-2131	Sequence 2131, Ap
4	27	37.5	9	3 US-09-641-528B-11725	Sequence 11725, A
5	27	37.5	9	3 US-09-641-528B-24500	Sequence 24500, A
6	27	37.5	10	3 US-09-641-528B-2132	Sequence 2132, Ap
7	27	37.5	10	3 US-09-641-528B-11726	Sequence 11726, A
8	27	37.5	10	3 US-09-641-528B-20365	Sequence 20365, A
9	27	37.5	10	3 US-09-641-528B-16759	Sequence 16759, A
10	27	37.5	11	3 US-09-641-528B-20366	Sequence 20366, A
11	27	37.5	11	3 US-09-641-528B-24535	Sequence 24535, A
12	27	37.5	11	3 US-09-641-528B-46330	Sequence 46330, A
13	27	37.5	15	3 US-09-641-528B-51190	Sequence 51190, A
14	26	36.1	12	1 US-08-460-602A-34	Sequence 34, Appl
15	26	36.1	12	1 US-08-463-966A-34	Sequence 34, Appl
16	26	36.1	12	1 US-08-465-217A-34	Sequence 34, Appl
17	26	36.1	12	1 US-08-464-329A-34	Sequence 34, Appl
18	26	36.1	12	1 US-08-462-507A-34	Sequence 34, Appl
19	26	36.1	12	1 US-08-467-881A-34	Sequence 34, Appl
20	26	36.1	12	1 US-08-563-222C-35	Sequence 35, Appl
21	26	36.1	12	2 US-09-563-222C-35	Sequence 35, Appl
22	26	36.1	15	2 US-10-198-053-500	Sequence 500, App
23	26	36.1	15	2 PCT-US93-11703-51	Sequence 51, Appl
24	26	36.1	15	5 PCT-US93-11703-52	Sequence 52, Appl
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102	25	34.7	9	2	US-09-073-138-99	Sequence 99, Appl	175	24	33.3	11	2	US-09-820-053A-127	Sequence 127, App
103	25	34.7	9	2	US-09-073-138-100	Sequence 100, App	176	24	33.3	12	1	US-08-031-148-10	Sequence 10, Appl
104	25	34.7	9	2	US-09-073-138-101	Sequence 101, App	177	24	33.3	12	1	US-08-031-148-11	Sequence 11, Appl
105	25	34.7	9	2	US-09-073-138-102	Sequence 102, App	178	24	33.3	12	2	US-08-415-838-10	Sequence 10, Appl
106	25	34.7	9	2	US-09-073-138-103	Sequence 103, App	179	24	33.3	12	2	US-08-415-838-11	Sequence 11, Appl
107	25	34.7	9	2	US-09-574-749B-28	Sequence 28, Appl	180	24	33.3	12	2	US-09-205-169-10	Sequence 10, Appl
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109	25	34.7	9	2	US-09-318-141-27	Sequence 27, Appl	182	24	33.3	13	2	US-08-908-469-60	Sequence 60, Appl
110	25	34.7	9	2	US-09-169-717B-33	Sequence 33, Appl	183	24	33.3	15	2	US-09-911-129B-14	Sequence 14, Appl
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113	25	34.7	9	2	US-09-806-769-27	Sequence 27, Appl	186	23	31.9	8	3	US-09-641-528B-6267	Sequence 6267, Ap
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116	25	34.7	9	2	US-09-862-260A-3	Sequence 3, Appl1	189	23	31.9	8	3	US-09-641-528B-20291	Sequence 20291, A
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131	25	34.7	9	2	US-09-898-860-93	Sequence 93, Appl	204	23	31.9	11	1	US-09-641-528B-42752	Sequence 42752, A
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134	25	34.7	9	2	US-09-898-860-96	Sequence 96, Appl	207	23	31.9	11	3	US-09-641-528B-10518	Sequence 10518, A
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137	25	34.7	9	2	US-09-898-860-99	Sequence 99, Appl	210	23	31.9	11	3	US-09-641-528B-42715	Sequence 42715, A
138	25	34.7	9	2	US-09-898-860-100	Sequence 100, App	211	23	31.9	12	2	US-09-563-222C-11	Sequence 11, Appl
139	25	34.7	9	2	US-09-898-860-101	Sequence 101, App	212	23	31.9	13	2	US-09-155-558-27	Sequence 27, Appl
140	25	34.7	9	2	US-09-898-860-102	Sequence 102, App	213	23	31.9	13	3	US-09-780-575A-5	Sequence 5, Appl1
141	25	34.7	9	2	US-09-898-860-103	Sequence 103, App	214	23	31.9	14	2	US-09-623-548A-1409	Sequence 1409, Ap
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147	25	34.7	9	3	US-09-641-528B-6268	Sequence 6268, Ap	220	23	31.9	15	2	US-08-837-058-23	Sequence 23, Appl
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158	25	34.7	10	3	US-09-641-528B-16619	Sequence 6269, Ap	231	22	30.6	8	3	US-09-641-528B-9438	Sequence 9438, Ap
159	25	34.7	10	3	US-09-641-528B-14612	Sequence 14612, A	232	22	30.6	8	3	US-09-641-528B-31529	Sequence 31529, A
160	25	34.7	10	3	US-09-641-528B-22568	Sequence 22568, A	233	22	30.6	8	3	US-09-641-528B-39799	Sequence 39799, A
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164	25	34.7	11	3	US-09-641-528B-17339	Sequence 17339, A	237	22	30.6	9	3	US-09-641-528B-26322	Sequence 26322, A
165	25	34.7	11	3	US-09-641-528B-22569	Sequence 22569, A	238	22	30.6	9	3	US-09-641-528B-26322	Sequence 26322, A
166	25	34.7	11	3	US-09-641-528B-27839	Sequence 27839, A	239	22	30.6	9	3	US-09-641-528B-28838	Sequence 28838, A
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168	25	34.7	11	3	US-09-641-528B-42858	Sequence 42858, A	241	22	30.6	9	3	US-09-641-528B-49040	Sequence 49040, A
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172	25	34.7	15	2	US-09-820-053A-152	Sequence 152, App	245	22	30.6	10	2	US-09-856-920-6	Sequence 6, Appl1

246	22	30.6	10	2	US-10-070-217-43	Sequence 43, Appl	319	21	29.2	9	3	US-09-641-528B-36453	Sequence 36453, A
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248	22	30.6	10	3	US-09-641-528B-7408	Sequence 7408, Ap	321	21	29.2	9	3	US-09-641-528B-43090	Sequence 43090, A
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251	22	30.6	10	3	US-09-641-528B-13110	Sequence 13110, A	324	21	29.2	9	3	US-09-641-528B-50050	Sequence 50050, A
252	22	30.6	10	3	US-09-641-528B-15822	Sequence 15822, A	325	21	29.2	9	3	US-09-641-528B-51012	Sequence 51012, A
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257	22	30.6	10	3	US-09-641-528B-39754	Sequence 39754, A	330	21	29.2	10	2	US-08-159-339A-605	Sequence 605, App
258	22	30.6	11	3	US-09-641-528B-7409	Sequence 7409, Ap	331	21	29.2	10	2	US-08-159-339A-141	Sequence 1041, App
259	22	30.6	11	3	US-09-641-528B-9390	Sequence 9390, Ap	332	21	29.2	10	2	US-09-358-020-21	Sequence 21, Appl
260	22	30.6	11	3	US-09-641-528B-9370	Sequence 9370, A	333	21	29.2	10	2	US-09-358-0430-498	Sequence 498, App
261	22	30.6	11	3	US-09-641-528B-39689	Sequence 39689, A	334	21	29.2	10	2	US-09-339-0430-1021	Sequence 1021, App
262	22	30.6	14	1	US-07-914-280-14	Sequence 14, Appl	335	21	29.2	10	2	US-09-339-0430-1163	Sequence 1163, Ap
263	22	30.6	14	5	PCT-US93-06625-14	Sequence 14, Appl	336	21	29.2	10	2	US-09-028-083B-33	Sequence 33, Appl
264	22	30.6	15	1	US-07-914-280-5	Sequence 5, Appl1	337	21	29.2	10	2	US-09-935-430-162	Sequence 162, App
265	22	30.6	15	1	US-08-129-607-1	Sequence 1, Appl1	338	21	29.2	10	2	US-09-935-430-262	Sequence 262, App
266	22	30.6	15	1	US-08-331-398A-36	Sequence 36, Appl	339	21	29.2	10	2	US-09-935-430-420	Sequence 420, App
267	22	30.6	15	1	US-08-331-397B-36	Sequence 36, Appl	340	21	29.2	10	2	US-09-698-3281-8	Sequence 8, Appl1
268	22	30.6	15	1	US-08-759-804A-36	Sequence 36, Appl	341	21	29.2	10	3	US-09-641-528B-5541	Sequence 5541, Ap
269	22	30.6	15	2	US-08-743-168B-13	Sequence 13, Appl	342	21	29.2	10	3	US-09-641-528B-10583	Sequence 10583, A
270	22	30.6	15	2	US-09-227-693-36	Sequence 36, Appl	343	21	29.2	10	3	US-09-641-528B-14160	Sequence 14160, A
271	22	30.6	15	2	US-09-623-548A-1244	Sequence 1244, Ap	344	21	29.2	10	3	US-09-641-528B-17377	Sequence 17377, A
272	22	30.6	15	2	US-09-657-276-1244	Sequence 1244, Ap	345	21	29.2	10	3	US-09-641-528B-17555	Sequence 17555, A
273	22	30.6	15	3	US-09-641-528B-46357	Sequence 46357, A	346	21	29.2	10	3	US-09-641-528B-27316	Sequence 27316, A
274	22	30.6	15	3	US-09-641-528B-46769	Sequence 46769, A	347	21	29.2	10	3	US-09-641-528B-28191	Sequence 28191, A
275	22	30.6	15	3	US-09-641-528B-46924	Sequence 46924, A	348	21	29.2	10	3	US-09-641-528B-29050	Sequence 29050, A
276	22	30.6	15	3	US-09-641-528B-46943	Sequence 46943, A	349	21	29.2	10	3	US-09-641-528B-36143	Sequence 36143, A
277	22	30.6	15	3	US-09-641-528B-47874	Sequence 47874, A	350	21	29.2	10	3	US-09-641-528B-36500	Sequence 36500, A
278	22	30.6	15	3	US-09-641-528B-47908	Sequence 47908, A	351	21	29.2	10	3	US-09-641-528B-37769	Sequence 37769, A
279	22	30.6	15	3	US-09-641-528B-48029	Sequence 48029, A	352	21	29.2	10	3	US-09-641-528B-42879	Sequence 42879, A
280	22	30.6	15	3	US-09-641-528B-48045	Sequence 48045, A	353	21	29.2	10	3	US-09-641-528B-42879	Sequence 42879, A
281	22	30.6	15	3	US-09-641-528B-50628	Sequence 50628, A	354	21	29.2	10	3	US-09-641-528B-43134	Sequence 43134, A
282	22	30.6	15	3	US-09-641-528B-50798	Sequence 50798, A	355	21	29.2	10	3	US-09-641-528B-43924	Sequence 43924, A
283	22	30.6	15	5	PCT-US92-08257-11	Sequence 11, Appl	356	21	29.2	11	1	PCT-US95-11126-21	Sequence 21, Appl
284	22	30.6	15	5	PCT-US93-06625-5	Sequence 5, Appl1	357	21	29.2	11	1	US-08-066-299-1	Sequence 1, Appl1
285	22	30.6	15	5	PCT-US94-00190-1	Sequence 1, Appl1	358	21	29.2	11	1	US-08-265-047-5	Sequence 5, Appl1
286	22	30.6	15	5	PCT-US96-10435-13	Sequence 13, Appl	359	21	29.2	11	1	US-08-048-979A-1	Sequence 1, Appl1
287	21	29.2	6	1	US-08-482-228-184	Sequence 184, App	360	21	29.2	11	2	US-09-339-043D-241	Sequence 241, App
288	21	29.2	7	2	US-08-482-528-184	Sequence 184, App	361	21	29.2	11	2	US-09-339-043D-510	Sequence 510, App
289	21	29.2	6	2	US-09-101-059-26	Sequence 26, Appl	362	21	29.2	11	2	US-09-239-043D-1030	Sequence 1030, Ap
290	21	29.2	8	1	US-08-922-267A-62	Sequence 62, Appl	363	21	29.2	11	2	US-09-239-043D-1371	Sequence 1371, Ap
291	21	29.2	8	1	US-08-685-152-5	Sequence 5, Appl1	364	21	29.2	11	2	US-08-657-749D-30	Sequence 30, Appl
292	21	29.2	8	2	US-09-060-011-4	Sequence 4, Appl1	365	21	29.2	11	3	US-09-641-528B-11005	Sequence 11005, A
293	21	29.2	8	2	US-09-573-497-4	Sequence 4, Appl1	366	21	29.2	11	3	US-09-641-528B-11039	Sequence 11039, A
294	21	29.2	8	2	US-09-415-640-5	Sequence 5, Appl1	367	21	29.2	11	3	US-09-641-528B-14941	Sequence 14941, A
295	21	29.2	8	2	US-09-306-542A-25	Sequence 25, Appl	368	21	29.2	11	3	US-09-641-528B-17558	Sequence 17558, A
296	21	29.2	8	2	US-09-239-043D-240	Sequence 240, App	369	21	29.2	11	3	US-09-641-528B-29093	Sequence 29093, A
297	21	29.2	8	2	US-09-239-043D-1370	Sequence 1370, App	370	21	29.2	11	3	US-09-641-528B-31661	Sequence 31661, A
298	21	29.2	8	2	US-10-050-271-4	Sequence 4, Appl1	371	21	29.2	11	3	US-09-641-528B-35501	Sequence 35501, A
299	21	29.2	8	2	US-09-756-283A-88	Sequence 88, Appl1	372	21	29.2	11	3	US-09-641-528B-37770	Sequence 37770, A
300	21	29.2	8	3	US-09-641-528B-6283	Sequence 6283, Ap	373	21	29.2	11	3	US-09-641-528B-37839	Sequence 37839, A
301	21	29.2	8	3	US-09-641-528B-11004	Sequence 11004, A	374	21	29.2	11	3	US-09-641-528B-43925	Sequence 43925, A
302	21	29.2	8	3	US-09-641-528B-17376	Sequence 17376, A	375	21	29.2	11	3	US-09-641-528B-43984	Sequence 43984, A
303	21	29.2	8	3	US-09-641-528B-22604	Sequence 22604, A	376	21	29.2	11	3	PCT-US94-04119-1	Sequence 45938, A
304	21	29.2	8	3	US-09-641-528B-28190	Sequence 28190, A	377	21	29.2	11	5	US-08-439-114-4	Sequence 1, Appl1
305	21	29.2	8	3	US-09-641-528B-28190	Sequence 28190, A	378	21	29.2	12	1	US-08-802-981-47	Sequence 4, Appl1
306	21	29.2	8	3	US-09-641-528B-37767	Sequence 37767, A	379	21	29.2	12	2	US-09-242-43-16	Sequence 16, Appl
307	21	29.2	8	3	US-09-641-528B-43104	Sequence 43104, A	380	21	29.2	12	2	US-09-394-019C-10	Sequence 10, Appl
308	21	29.2	9	1	US-09-641-528B-43923	Sequence 43923, A	381	21	29.2	12	2	US-09-644-668A-17	Sequence 17, Appl
309	21	29.2	9	1	US-08-417-174-124	Sequence 124, App	382	21	29.2	12	2	US-09-820-078A-67	Sequence 67, Appl
310	21	29.2	9	2	US-09-267-439-124	Sequence 124, App	383	21	29.2	12	2	US-09-747-287A-45	Sequence 45, Appl
311	21	29.2	9	2	US-09-073-138-124	Sequence 124, App	384	21	29.2	12	2	US-09-665-819A-16	Sequence 16, Appl
312	21	29.2	9	3	US-09-898-860-124	Sequence 124, App	385	21	29.2	12	2	US-09-394-019C-10	Sequence 10, Appl
313	21	29.2	9	3	US-09-641-528B-6284	Sequence 6284, Ap	386	21	29.2	12	5	US-09-644-668A-17	Sequence 17, Appl
314	21	29.2	9	3	US-09-641-528B-7743	Sequence 7743, Ap	387	21	29.2	13	1	PCT-US95-00605-17	Sequence 21, Appl
315	21	29.2	9	3	US-09-641-528B-14940	Sequence 14940, A	388	21	29.2	13	1	US-08-189-777-2	Sequence 2, Appl1
316	21	29.2	9	3	US-09-641-528B-17252	Sequence 17252, A	389	21	29.2	13	1	US-08-188-277B-11	Sequence 11, Appl
317	21	29.2	9	3	US-09-641-528B-22605	Sequence 22605, A	390	21	29.2	13	2	US-09-234-163-13	Sequence 13, Appl
318	21	29.2	9	3	US-09-641-528B-27385	Sequence 27385, A	391	21	29.2	13	2	US-08-901-379-13	Sequence 13, Appl
					US-09-641-528B-29049	Sequence 29049, A						US-09-820-053A-35	Sequence 35, Appl

392	21	29.2	13	2	US-09-820-053A-157	Sequence 157, App	465	20	27.8	9	2	US-08-159-339A-1019	Sequence 1019, Ap
393	21	29.2	13	2	US-09-848-107A-7	Sequence 7, Appl1	466	20	27.8	9	2	US-09-267-439-67	Sequence 67, Appl
394	21	29.2	14	1	US-07-745-382-2	Sequence 2, Appl1	467	20	27.8	9	2	US-09-492-543-187	Sequence 187, App
395	21	29.2	14	1	US-07-921-848-2	Sequence 2, Appl1	468	20	27.8	9	2	US-09-073-138-67	Sequence 67, Appl
396	21	29.2	14	1	US-08-201-046A-25	Sequence 25, Appl1	469	20	27.8	9	2	US-09-631-863A-75	Sequence 75, Appl
397	21	29.2	14	1	US-08-260-086-4	Sequence 4, Appl1	470	20	27.8	9	2	US-09-935-430-560	Sequence 560, App
398	21	29.2	14	1	US-08-165-301A-2	Sequence 2, Appl1	471	20	27.8	9	2	US-09-865-546A-204	Sequence 204, App
399	21	29.2	14	1	US-08-188-277B-24	Sequence 24, Appl1	472	20	27.8	9	2	US-10-172-597-187	Sequence 187, App
400	21	29.2	14	2	US-09-461-697-391	Sequence 2, Appl1	473	20	27.8	9	2	US-09-898-860-67	Sequence 67, Appl
401	21	29.2	14	2	US-08-810-436-2	Sequence 391, App	474	20	27.8	9	3	US-09-641-528B-3598	Sequence 3598, Ap
402	21	29.2	14	2	US-09-242-435-17	Sequence 17, Appl1	475	20	27.8	9	3	US-09-641-528B-7605	Sequence 7605, Ap
403	21	29.2	14	2	US-08-671-548C-73	Sequence 73, Appl	476	20	27.8	9	3	US-09-641-528B-12766	Sequence 12766, A
404	21	29.2	14	2	US-09-116-676-4	Sequence 4, Appl1	477	20	27.8	9	3	US-09-641-528B-15543	Sequence 15543, A
405	21	29.2	14	2	US-08-284-667A-73	Sequence 73, Appl1	478	20	27.8	9	3	US-09-641-528B-16840	Sequence 16840, A
406	21	29.2	14	5	PCT-US94-14179-2	Sequence 73, Appl1	479	20	27.8	9	3	US-09-641-528B-25158	Sequence 25158, A
407	21	29.2	14	5	US-08-201-046A-24	Sequence 2, Appl1	480	20	27.8	9	3	US-09-641-528B-25667	Sequence 25667, A
408	21	29.2	15	1	US-08-218-025A-19	Sequence 24, Appl1	481	20	27.8	9	3	US-09-641-528B-28956	Sequence 28956, A
409	21	29.2	15	1	US-08-218-025A-19	Sequence 179, App	482	20	27.8	9	3	US-09-641-528B-48685	Sequence 48685, A
410	21	29.2	15	1	US-08-118-025A-193	Sequence 193, App	483	20	27.8	9	3	US-09-641-528B-50903	Sequence 50903, A
411	21	29.2	15	1	US-08-394-004-1	Sequence 1, Appl1	484	20	27.8	9	5	PCT-US95-04975-4	Sequence 4, Appl1
412	21	29.2	15	1	US-08-267-092A-61	Sequence 61, Appl1	485	20	27.8	10	1	US-08-166-195A-7	Sequence 7, Appl1
413	21	29.2	15	1	US-08-095-332-7	Sequence 7, Appl1	486	20	27.8	10	1	US-08-131-057A-7	Sequence 7, Appl1
414	21	29.2	15	1	US-08-195-874-2	Sequence 2, Appl1	487	20	27.8	10	1	US-08-436-772-3	Sequence 3, Appl1
415	21	29.2	15	1	US-07-760-530-7	Sequence 7, Appl1	488	20	27.8	10	1	US-08-436-883B-3	Sequence 3, Appl1
416	21	29.2	15	1	US-08-540-412-63	Sequence 63, Appl1	489	20	27.8	10	2	US-09-649-063-13	Sequence 13, Appl1
417	21	29.2	15	1	US-07-847-311A-7	Sequence 7, Appl1	490	20	27.8	10	2	US-10-365-908-73	Sequence 73, Appl1
418	21	29.2	15	1	US-08-484-905-26	Sequence 26, Appl1	491	20	27.8	10	2	US-09-935-430-417	Sequence 417, App
419	21	29.2	15	2	US-08-986-234-27	Sequence 27, Appl1	492	20	27.8	10	2	US-09-935-430-518	Sequence 518, App
420	21	29.2	15	2	US-08-481-985B-36	Sequence 26, Appl1	493	20	27.8	10	2	US-09-820-053A-142	Sequence 142, App
421	21	29.2	15	2	US-09-051-342-63	Sequence 63, Appl1	494	20	27.8	10	2	US-10-070-217-38	Sequence 38, Appl
422	21	29.2	15	2	US-08-468-161-63	Sequence 21, Appl1	495	20	27.8	10	2	US-10-070-217-49	Sequence 49, Appl
423	21	29.2	15	2	US-08-370-476-26	Sequence 26, Appl1	496	20	27.8	10	2	US-08-908-469-95	Sequence 95, Appl
424	21	29.2	15	2	US-09-051-759-63	Sequence 63, Appl1	497	20	27.8	10	2	US-10-057-788-121	Sequence 121, App
425	21	29.2	15	2	US-09-255-668-2	Sequence 2, Appl1	498	20	27.8	10	3	US-09-641-528B-2688	Sequence 2688, Ap
426	21	29.2	15	2	US-08-060-988A-41	Sequence 41, Appl1	499	20	27.8	10	3	US-09-641-528B-3479	Sequence 3479, Ap
427	21	29.2	15	2	US-09-310-187A-3	Sequence 3, Appl1	500	20	27.8	10	3	US-09-641-528B-3599	Sequence 3599, Ap
428	21	29.2	15	2	US-08-669-656A-21	Sequence 21, Appl1	501	20	27.8	10	3	US-09-641-528B-7492	Sequence 7492, Ap
429	21	29.2	15	2	US-09-787-140-2	Sequence 102, App	502	20	27.8	10	3	US-09-641-528B-7606	Sequence 7606, Ap
430	21	29.2	15	2	US-09-069-827A-102	Sequence 102, App	503	20	27.8	10	3	US-09-641-528B-12147	Sequence 12147, Ap
431	21	29.2	15	2	US-09-239-043D-2080	Sequence 2080, Ap	504	20	27.8	10	3	US-09-641-528B-12673	Sequence 12673, A
432	21	29.2	15	2	US-09-239-043D-2083	Sequence 2080, Ap	505	20	27.8	10	3	US-09-641-528B-12767	Sequence 12767, A
433	21	29.2	15	2	US-09-239-043D-2215	Sequence 2215, Ap	506	20	27.8	10	3	US-09-641-528B-15459	Sequence 15459, A
434	21	29.2	15	2	US-09-160-076-2	Sequence 2, Appl1	507	20	27.8	10	3	US-09-641-528B-15544	Sequence 15544, A
435	21	29.2	15	2	US-09-820-053A-43	Sequence 43, Appl1	508	20	27.8	10	3	US-09-641-528B-21060	Sequence 21060, A
436	21	29.2	15	2	US-10-339-160-2	Sequence 46361, A	509	20	27.8	10	3	US-09-641-528B-23240	Sequence 23240, A
437	21	29.2	15	3	US-09-641-528B-47356	Sequence 46361, A	510	20	27.8	10	3	US-09-641-528B-24970	Sequence 24970, A
438	21	29.2	15	3	US-09-641-528B-47369	Sequence 47356, A	511	20	27.8	10	3	US-09-641-528B-25668	Sequence 25668, A
439	21	29.2	15	3	US-09-641-528B-47658	Sequence 47658, A	512	20	27.8	10	3	US-09-641-528B-28957	Sequence 28957, A
440	21	29.2	15	3	US-09-641-528B-47669	Sequence 47669, A	513	20	27.8	11	1	US-07-912-900-14	Sequence 14, Appl1
441	21	29.2	15	3	US-09-641-528B-47673	Sequence 47673, A	514	20	27.8	11	1	US-08-082-844-6	Sequence 6, Appl1
442	21	29.2	15	3	US-09-641-528B-47673	Sequence 47673, A	515	20	27.8	11	1	US-08-285-309-14	Sequence 14, Appl1
443	21	29.2	15	3	US-09-641-528B-47953	Sequence 47953, A	516	20	27.8	11	1	US-08-313-075A-13	Sequence 13, Appl1
444	21	29.2	15	3	US-09-641-528B-47969	Sequence 47969, A	517	20	27.8	11	1	US-08-432-694-2	Sequence 2, Appl1
445	21	29.2	15	3	US-09-641-528B-47977	Sequence 47977, A	518	20	27.8	11	1	US-08-432-694-4	Sequence 4, Appl1
446	21	29.2	15	3	US-09-641-528B-50681	Sequence 50681, A	519	20	27.8	11	1	US-08-549-008-48	Sequence 48, Appl1
447	21	29.2	15	3	US-09-641-528B-50730	Sequence 50730, A	520	20	27.8	11	1	US-08-549-008-50	Sequence 50, Appl1
448	21	29.2	15	3	US-09-641-528B-51186	Sequence 51186, A	521	20	27.8	11	1	US-08-502-046-14	Sequence 14, Appl1
449	21	29.2	15	3	US-09-947-770-21	Sequence 21, Appl1	522	20	27.8	11	2	US-08-802-981-145	Sequence 145, App
450	21	29.2	15	5	PCT-US93-11703-56	Sequence 56, Appl1	523	20	27.8	11	2	US-08-802-981-153	Sequence 153, App
451	21	29.2	15	5	PCT-US95-01671-3	Sequence 2, Appl1	524	20	27.8	11	2	US-08-802-981-155	Sequence 155, App
452	21	29.2	15	5	PCT-US95-08156-63	Sequence 63, Appl1	525	20	27.8	11	2	US-08-974-549A-63	Sequence 63, App
453	21	29.2	7	2	US-09-209-676-19	Sequence 19, Appl1	526	20	27.8	11	2	US-09-317-926-2	Sequence 2, Appl1
454	20	27.8	6	2	US-08-318-856A-29	Sequence 29, Appl1	527	20	27.8	11	2	US-08-912-951-63	Sequence 63, Appl1
455	20	27.8	8	1	US-08-925-002-17	Sequence 17, Appl1	528	20	27.8	11	2	US-09-402-181B-63	Sequence 63, Appl1
456	20	27.8	8	2	US-08-197-484-19	Sequence 19, Appl1	529	20	27.8	11	2	US-09-721-456-63	Sequence 63, Appl1
457	20	27.8	8	2	US-09-910-552-17	Sequence 17, Appl1	530	20	27.8	11	2	US-09-284-100A-16	Sequence 16, Appl1
458	20	27.8	8	2	US-09-454-204A-2	Sequence 2, Appl1	531	20	27.8	11	2	US-09-747-287A-214	Sequence 214, App
459	20	27.8	8	2	US-09-454-204A-2	Sequence 22, Appl1	532	20	27.8	11	2	US-09-747-287A-219	Sequence 219, App
460	20	27.8	8	2	US-09-454-204A-22	Sequence 10, Appl1	533	20	27.8	11	2	US-09-394-019C-168	Sequence 168, App
461	20	27.8	8	2	US-09-763-397A-10	Sequence 10, Appl1	534	20	27.8	11	2	US-09-394-019C-173	Sequence 173, App
462	20	27.8	9	5	PCT-US95-02121-19	Sequence 19, Appl1	535	20	27.8	11	3	US-09-641-528B-3480	Sequence 3480, Ap
463	20	27.8	9	1	US-08-417-174-67	Sequence 67, Appl1	536	20	27.8	11	3	US-09-641-528B-3554	Sequence 3554, Ap
464	20	27.8	9	1	US-08-318-856A-45	Sequence 45, Appl1	537	20	27.8	11	3	US-09-641-528B-7493	Sequence 7493, Ap

538	20	27.8	11	3	US-09-641-5288-7566	Sequence 7566, Ap	611	20	27.8	15	2	US-09-382-265B-6	Sequence 6, Appl
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RESULT 1
US-09-185-501B-6
; Sequence 6, Application US/09185501B
; Patent No. 6311428
GENERAL INFORMATION:
; APPLICANT: KATO, NOBUO
; TITLE OF INVENTION: HEXULOSE PHOSPHATE ISOMERASE GENE
; FILE REFERENCE: 0010-0953-OCIP
; CURRENT APPLICATION NUMBER: JP9-231131
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; LENGTH: 12
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US-09-185-501B-6

ALIGNMENTS

Query Match 50.0%; Score 36; DB 2; Length 12;
Best Local Similarity 80.0%; Pred. No. 4.9;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 3 VPSVAGVK 12

RESULT 2

US-09-305-781-2
; Sequence 2, Application US/09305781
; Patent No. 6358511
; GENERAL INFORMATION:
; APPLICANT: Klocman et al.
; TITLE OF INVENTION: NOVEL INHIBITORS OF HIV INFECTION
; FILE REFERENCE: 070165.0454
; CURRENT APPLICATION NUMBER: US/09/305,781
; CURRENT FILING DATE: 1999-05-03
; EARLIER APPLICATION NUMBER: 60/084,076
; EARLIER FILING DATE: 1998-05-04
; NUMBER OF SEQ. ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Human
US-09-305-781-2

Query Match 38.2%; Score 27.5; DB 2; Length 14;
Best Local Similarity 69.2%; Pred. No. 2e+02;
Matches 9; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 1 VPSVAKSVKSLV 13
|:|:|:|:|:
DB 3 VEASVA-SVRSLY 14

RESULT 3

US-09-641-528B-2131
; Sequence 2131, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ. ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2131
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-2131

Query Match 37.5%; Score 27; DB 3; Length 9;
Best Local Similarity 55.6%; Pred. No. 5e+05;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 SVAKSVKSL 12
|:|:|:|:|:
DB 1 SIADSIKTL 9

RESULT 4
US-09-641-528B-11725
; Sequence 11725, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ. ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11725
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-11725

Query Match 37.5%; Score 27; DB 3; Length 9;
Best Local Similarity 55.6%; Pred. No. 5e+05;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 SVAKSVKSL 12
|:|:|:|:|:
DB 1 SIADSIKTL 9

RESULT 5
US-09-641-528B-24500
; Sequence 24500, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ. ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24500
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-24500

Query Match 37.5%; Score 27; DB 3; Length 9;
Best Local Similarity 55.6%; Pred. No. 5e+05;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 SVAKSVKSL 12
|:|:|:|:|:
DB 1 SIADSIKTL 9

Db 1 SIADSIKTL 9

```
RESULT 6
US-09-641-528B-2132
; Sequence 2132, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2132
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-2132
```

```
Query Match 37.5%; Score 27; DB 3; Length 10;
Best Local Similarity 55.6%; Pred. No. 1.7e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

QY 4 SVAKSYSKL 12
Db 1 SIADSIKTL 9

```
RESULT 7
US-09-641-528B-11726
; Sequence 11726, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11726
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-11726
```

```
Query Match 37.5%; Score 27; DB 3; Length 10;
Best Local Similarity 55.6%; Pred. No. 1.7e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

QY 4 SVAKSYSKL 12

Db 1 SIADSIKTL 9

```
RESULT 8
US-09-641-528B-20365
; Sequence 20365, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20365
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-20365
```

```
Query Match 37.5%; Score 27; DB 3; Length 10;
Best Local Similarity 55.6%; Pred. No. 1.7e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

QY 4 SVAKSYSKL 12
Db 2 SIADSIKTL 10

```
RESULT 9
US-09-641-528B-24501
; Sequence 24501, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24501
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-24501
```

```
Query Match 37.5%; Score 27; DB 3; Length 10;
Best Local Similarity 55.6%; Pred. No. 1.7e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

QY 4 SVAKSVKSL 12
|:|:|:|
Db 1 S1ADS1K1TL 9

RESULT 10

US-09-641-528B-16759
; Sequence 16759, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16759
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-16759

Query Match 37.5%; Score 27; DB 3; Length 11;
Best Local Similarity 55.6%; Pred. No. 1.9e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 SVAKSVKSL 12
|:|:|:|
Db 3 S1ADS1K1TL 11

RESULT 11

US-09-641-528B-20366
; Sequence 20366, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20366
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-20366

Query Match 37.5%; Score 27; DB 3; Length 11;
Best Local Similarity 55.6%; Pred. No. 1.9e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 SVAKSVKSL 12
|:|:|:|
Db 2 S1ADS1K1TL 10

RESULT 12

US-09-641-528B-24535
; Sequence 24535, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24535
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-24535

Query Match 37.5%; Score 27; DB 3; Length 11;
Best Local Similarity 55.6%; Pred. No. 1.9e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 SVAKSVKSL 12
|:|:|:|
Db 3 S1ADS1K1TL 11

RESULT 13

US-09-641-528B-46330
; Sequence 46330, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46330
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-46330

Query Match 37.5%; Score 27; DB 3; Length 15;
Best Local Similarity 55.6%; Pred. No. 2.7e+02;

Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 SVAKSVKSL 12
|:|:|:|
Db 7 SIADSIKTL 15

RESULT 14
US-09-641-528B-51190
; Sequence 51190, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51190
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-51190

Query Match 37.5%; Score 27; DB 3; Length 15;
Best Local Similarity 55.6%; Pred. No. 2.7e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 SVAKSVKSL 12
|:|:|:|
Db 3 SIADSIKTL 11

RESULT 15
US-08-257-528B-34
; Sequence 34, Application US/08257528B
; Patent No. 5639854
; GENERAL INFORMATION:
; APPLICANT: SIA, Charles D.Y.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/257,528B
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, MICHAEL I.
; REGISTRATION NUMBER: 24,973

; REFERENCE/DOCKET NUMBER: 1038-336 MIS.:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-257-528B-34

Query Match 36.1%; Score 26; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 KSIYLG 15
|:|:|
Db 2 KSIYIG 7

RESULT 16
US-08-460-602A-34
; Sequence 34, Application US/08460602A
; Patent No. 5759769
; GENERAL INFORMATION:
; APPLICANT: SIA, Charles D.Y.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,602A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/257,528
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/073,378
; FILING DATE: 09-JUN-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, MICHAEL I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-450 MIS.:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-460-602A-34

Query Match 36.1%; Score 26; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 KSLYLG 15
||:|:
Db 2 KSIYIG 7

RESULT 17
US-08-463-966A-34
; Sequence 34, Application US/08463966A
; Patent No. 5795955
; GENERAL INFORMATION:
; APPLICANT: SIA, Charles D.Y.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,966A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/257,528
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/073,378
; FILING DATE: 09-JUN-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, MICHAEL I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-487 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-463-966A-34

Query Match 36.1%; Score 26; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 KSLYLG 15
||:|:
Db 2 KSIYIG 7

RESULT 18
US-08-465-217A-34
; Sequence 34, Application US/08465217A
; Patent No. 5800822
; GENERAL INFORMATION:
; APPLICANT: SIA, Charles D.Y.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides

; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,217A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/257,528
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/073,378
; FILING DATE: 09-JUN-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, MICHAEL I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-486 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-465-217A-34

Query Match 36.1%; Score 26; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 KSLYLG 15
||:|:
Db 2 KSIYIG 7

RESULT 19
US-08-464-329A-34
; Sequence 34, Application US/08464329A
; Patent No. 5817754
; GENERAL INFORMATION:
; APPLICANT: SIA, Charles D.Y.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,329A

FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-449 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-464-329A-34

Query Match 36.1%; Score 26; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 KSLYIG 15
DB 2 KSLYIG 7

RESULT 20
US-08-462-507A-34
Sequence 34, Application US/08462507A
Patent No. 5876731
GENERAL INFORMATION:
APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,507A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-451 MIS:jb
TELECOMMUNICATION INFORMATION:

TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-462-507A-34

Query Match 36.1%; Score 26; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 KSLYIG 15
DB 2 KSLYIG 7

RESULT 21
US-08-467-881A-34
Sequence 34, Application US/08467881A
Patent No. 5951986
GENERAL INFORMATION:
APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,881A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-488 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-467-881A-34

Query Match 36.1%; Score 26; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 KSLYIG 15

Db 2 KSIYIG 7

RESULT 22

US-09-563-222C-35
Sequence 35, Application US/09563222C
Patent No. 6696620
GENERAL INFORMATION:
APPLICANT: EPICYTE PHARMACEUTICALS, INC.
APPLICANT: HIATT, ANDREW C.
APPLICANT: HEIN, MICH B.
TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
FILE REFERENCE: 068904-0501
CURRENT APPLICATION NUMBER: US/09/563,222C
CURRENT FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: PCT/US01/14349
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 09/563,222
PRIOR FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 182
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 35
LENGTH: 12
TYPE: PRT
ORGANISM: Mus musculus
US-09-563-222C-35

Query Match 36.1%; Score 26; DB 2; Length 12;
Best Local Similarity 54.5%; Pred. No. 3.2e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 SVAKSVKSLYL 14
Db 1 SASSSVSSYL 11

RESULT 23

US-08-218-025A-183
Sequence 183, Application US/08218025A
Patent No. 5556744
GENERAL INFORMATION:
APPLICANT: Weiner, David B.
APPLICANT: Ugen, Kenneth E.
APPLICANT: Williams, William V.
TITLE OF INVENTION: Methods and Compositions for Diagnosing
TITLE OF INVENTION: and Treating Certain HIV Infected Patients
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: P.O. Box 457, 321 No. 55567441sttown Road
CITY: Spring House
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/218,025A
FILING DATE: 24-MAR-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/891,451
FILING DATE: 29-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WSTJ3A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 540-9206

TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 183:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-218-025A-183

Query Match 36.1%; Score 26; DB 1; Length 15;
Best Local Similarity 66.7%; Pred. No. 4.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 KSLYIG 15
Db 1 KSIYIG 6

RESULT 24

US-10-198-053-500
Sequence 500, Application US/10198053
Patent No. 6858710
GENERAL INFORMATION:
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary R.
APPLICANT: Hill, Paul
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C9
CURRENT APPLICATION NUMBER: US/10/198,053
CURRENT FILING DATE: 2002-07-17
NUMBER OF SEQ ID NOS: 624
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 500
LENGTH: 15
TYPE: PRT
ORGANISM: Homo sapiens
US-10-198-053-500

Query Match 36.1%; Score 26; DB 2; Length 15;
Best Local Similarity 53.8%; Pred. No. 4.1e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY 2 PFSVAKSVKSLYL 14
Db 2 PYSLDK--SLYL 12

RESULT 25

PCT-US93-11703-51
Sequence 51, Application PC/TUS9311703
GENERAL INFORMATION:
APPLICANT: Chiron Mimotopes Pty. Ltd.
TITLE OF INVENTION: T-Cell Epitopes
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Grant D. Green
STREET: 4560 Horton St.
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11703
FILING DATE: 28-DEC-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/984,852
FILING DATE: 02-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Green, Grant D.
REGISTRATION NUMBER: 31,259
REFERENCE/DOCKET NUMBER: 0222.101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2706
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-11703-51

Query Match 36.1%; Score 26; DB 5; Length 15;
Best Local Similarity 66.7%; Pred. No. 4.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 KSLVIG 15
DB 10 KSIYIG 15

RESULT 26
PCT-US93-11703-52
Sequence 52, Application PC/TUS9311703
GENERAL INFORMATION:
APPLICANT: Chiron Mimotopes Pty. Ltd.
TITLE OF INVENTION: T-Cell Epitopes
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Grant D. Green
STREET: 4560 Horton St.
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11703
FILING DATE: 28-DEC-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/984,852
FILING DATE: 02-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Green, Grant D.
REGISTRATION NUMBER: 31,259
REFERENCE/DOCKET NUMBER: 0222.101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2706
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-11703-52

Query Match 36.1%; Score 26; DB 5; Length 15;
Best Local Similarity 66.7%; Pred. No. 4.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 KSLVIG 15
DB 8 KSIYIG 13

RESULT 27
PCT-US93-11703-53
Sequence 53, Application PC/TUS9311703
GENERAL INFORMATION:
APPLICANT: Chiron Mimotopes Pty. Ltd.
TITLE OF INVENTION: T-Cell Epitopes
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Grant D. Green
STREET: 4560 Horton St.
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11703
FILING DATE: 28-DEC-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/984,852
FILING DATE: 02-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Green, Grant D.
REGISTRATION NUMBER: 31,259
REFERENCE/DOCKET NUMBER: 0222.101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2706
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-11703-53

Query Match 36.1%; Score 26; DB 5; Length 15;
Best Local Similarity 66.7%; Pred. No. 4.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 KSLVIG 15
DB 6 KSIYIG 11

RESULT 28
PCT-US93-11703-54
Sequence 54, Application PC/TUS9311703
GENERAL INFORMATION:
APPLICANT: Chiron Mimotopes Pty. Ltd.
TITLE OF INVENTION: T-Cell Epitopes
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Grant D. Green
STREET: 4560 Horton St.
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.308
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11703
FILING DATE: 28-DEC-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/984,852
FILING DATE: 02-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Green, Grant D.
REGISTRATION NUMBER: 31,259
REFERENCE/DOCKET NUMBER: 0222.101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2706
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-11703-54

Query Match 36.1%; Score 26; DB 5; Length 15;
Best Local Similarity 66.7%; Pred. No. 4.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 KSLYLIG 15
||:|:
Db 4 KSIYIG 9

RESULT 29
PCT-US93-11703-55
Sequence 55, Application PC/TUS9311703
GENERAL INFORMATION:
APPLICANT: Chilton Mimotopes Pty. Ltd.
TITLE OF INVENTION: T-Cell Epitopes
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Grant D. Green
STREET: 4560 Horton St.
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.308
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11703
FILING DATE: 28-DEC-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/984,852
FILING DATE: 02-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Green, Grant D.
REGISTRATION NUMBER: 31,259
REFERENCE/DOCKET NUMBER: 0222.101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2706
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
PCT-US93-11703-55

Query Match 36.1%; Score 26; DB 5; Length 15;
Best Local Similarity 66.7%; Pred. No. 4.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 KSLYLIG 15
||:|:
Db 2 KSIYIG 7

RESULT 30
US-08-787-547-62
Sequence 62, Application US/08787547
Patent No. 5783567
GENERAL INFORMATION:
APPLICANT: Hedley, Mary Lynne
APPLICANT: Curley, Joanne M.
APPLICANT: Langer, Robert S.
TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY
TITLE OF INVENTION: OF NUCLEIC ACID
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/787,547
FILING DATE: 22-JAN-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 08191/003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-787-547-62

Query Match 34.7%; Score 25; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPPSV 5
|||||
Db 5 VPPSV 9

RESULT 31
US-08-417-174-48
Sequence 48, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,

```
/
/ APPLICANT: STEVEN A.
/ TITLE OF INVENTION: MELANOMA ANTIGENS AND
/ THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
/ TITLE OF INVENTION: METHODS
/ NUMBER OF SEQUENCES: 126
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
/ STREET: 345 PARK AVENUE
/ CITY: NEW YORK
/ STATE: NEW YORK
/ COUNTRY: USA
/ ZIP: 10154
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: FLOPPY DISK
/ COMPUTER: IBM PC COMPATIBLE
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: ASCII
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/417,174
/ FILING DATE: 05-APR-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/231,565
/ FILING DATE: 22-APR-1994
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: CAROL M. GRUPPI
/ REGISTRATION NUMBER: 37,341
/ REFERENCE/DOCKET NUMBER: 2026-4124US1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 758-4800
/ TELEFAX: (212) 751-6849
/
/ INFORMATION FOR SEQ ID NO: 48:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 9
/ TYPE: amino acid
/ STRANDEDNESS: Unknown
/ TOPOLOGY: Unknown
/ MOLECULE TYPE: Peptide
/
/ US-08-417-174-48
/
/ Query Match
/ Best Local Similarity 34.7%; Score 25; DB 1; Length 9;
/ Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/
/ QY 1 VFPSV 5
/ Db 5 VFPSV 9
/
/ RESULT 32
/ US-08-417-174-83
/ Sequence 83, Application US/08417174
/ Patent No. 5844075
/
/ GENERAL INFORMATION:
/ APPLICANT: KAMAKAMI, YUTAKA; ROSENBERG,
/ APPLICANT: STEVEN A.
/ TITLE OF INVENTION: MELANOMA ANTIGENS AND
/ THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
/ TITLE OF INVENTION: METHODS
/ NUMBER OF SEQUENCES: 126
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
/ STREET: 345 PARK AVENUE
/ CITY: NEW YORK
/ STATE: NEW YORK
/ COUNTRY: USA
/ ZIP: 10154
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: FLOPPY DISK
/ COMPUTER: IBM PC COMPATIBLE
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: ASCII
```

```
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/417,174
/ FILING DATE: 05-APR-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/231,565
/ FILING DATE: 22-APR-1994
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: CAROL M. GRUPPI
/ REGISTRATION NUMBER: 37,341
/ REFERENCE/DOCKET NUMBER: 2026-4124US1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 758-4800
/ TELEFAX: (212) 751-6849
/
/ INFORMATION FOR SEQ ID NO: 83:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 9
/ TYPE: amino acid
/ STRANDEDNESS: Unknown
/ TOPOLOGY: Unknown
/ MOLECULE TYPE: Peptide
/
/ US-08-417-174-83
/
/ Query Match
/ Best Local Similarity 34.7%; Score 25; DB 1; Length 9;
/ Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/
/ QY 1 VFPSV 5
/ Db 5 VFPSV 9
/
/ RESULT 33
/ US-08-417-174-84
/ Sequence 84, Application US/08417174
/ Patent No. 5844075
/
/ GENERAL INFORMATION:
/ APPLICANT: KAMAKAMI, YUTAKA; ROSENBERG,
/ APPLICANT: STEVEN A.
/ TITLE OF INVENTION: MELANOMA ANTIGENS AND
/ THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
/ TITLE OF INVENTION: METHODS
/ NUMBER OF SEQUENCES: 126
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
/ STREET: 345 PARK AVENUE
/ CITY: NEW YORK
/ STATE: NEW YORK
/ COUNTRY: USA
/ ZIP: 10154
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: FLOPPY DISK
/ COMPUTER: IBM PC COMPATIBLE
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: ASCII
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/417,174
/ FILING DATE: 22-APR-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/231,565
/ FILING DATE: 05-APR-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: CAROL M. GRUPPI
/ REGISTRATION NUMBER: 37,341
/ REFERENCE/DOCKET NUMBER: 2026-4124US1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 758-4800
/ TELEFAX: (212) 751-6849
/
/ INFORMATION FOR SEQ ID NO: 84:
/ SEQUENCE CHARACTERISTICS:
```

LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-417-174-84

Query Match 34.7%; Score 25; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSV 5
|||
Db 5 VPFSV 9

RESULT 34
US-08-417-174-85
Sequence 85, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-417-174-85

Query Match 34.7%; Score 25; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSV 5
|||
Db 5 VPFSV 9

RESULT 35

US-08-417-174-86
Sequence 86, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.

TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-417-174-86

Query Match 34.7%; Score 25; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSV 5
|||
Db 5 VPFSV 9

RESULT 36
US-08-417-174-87
Sequence 87, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-417-174-87

Query Match
Best Local Similarity 34.7%; Score 25; DB 1; Length 9;
Matches 5; Conservativity 100.0%; Pred. No. 5e+05; Indels 0; Gaps 0;

QY 1 VPFSV 5
Db 5 VPFSV 9

RESULT 37
US-08-417-174-88
Sequence 88, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-417-174-88

Query Match
Best Local Similarity 34.7%; Score 25; DB 1; Length 9;
Matches 5; Conservativity 100.0%; Pred. No. 5e+05; Indels 0; Gaps 0;

QY 1 VPFSV 5
Db 5 VPFSV 9

RESULT 38
US-08-417-174-89
Sequence 89, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-417-174-89

Query Match
Best Local Similarity 34.7%; Score 25; DB 1; Length 9;
Matches 5; Conservativity 100.0%; Pred. No. 5e+05; Indels 0; Gaps 0;

QY 1 VPFSV 5

Db 5 VPFSV 9

RESULT 39

US-08-417-174-90

Sequence 90, Application US/08417174

Patent No. 5844075

GENERAL INFORMATION:

APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,

APPLICANT: STEVEN A.

TITLE OF INVENTION: MELANOMA ANTIGENS AND

TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC

NUMBER OF SEQUENCES: 126

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/417,174

FILING DATE: 05-APR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/231,565

FILING DATE: 22-APR-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: CAROL M. GRUPPI

REGISTRATION NUMBER: 37,341

REFERENCE/DOCKET NUMBER: 2026-4124US1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 758-4800

TELEFAX: (212) 751-6849

TELEX: 421792

INFORMATION FOR SEQ ID NO: 90:

SEQUENCE CHARACTERISTICS:

LENGTH: 9

TYPE: amino acid

STRANDEDNESS: Unknown

TOPOLOGY: Unknown

MOLECULE TYPE: Peptide

US-08-417-174-90

Query Match 34.7%; Score 25; DB 1; Length 9;

Best Local Similarity 100.0%; Pred. No. 5e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFSV 5

Db 5 VPFSV 9

RESULT 40

US-08-417-174-91

Sequence 91, Application US/08417174

Patent No. 5844075

GENERAL INFORMATION:

APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,

APPLICANT: STEVEN A.

TITLE OF INVENTION: MELANOMA ANTIGENS AND

TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC

NUMBER OF SEQUENCES: 126

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/417,174

FILING DATE: 05-APR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/231,565

FILING DATE: 22-APR-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: CAROL M. GRUPPI

REGISTRATION NUMBER: 37,341

REFERENCE/DOCKET NUMBER: 2026-4124US1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 758-4800

TELEFAX: (212) 751-6849

TELEX: 421792

INFORMATION FOR SEQ ID NO: 91:

SEQUENCE CHARACTERISTICS:

LENGTH: 9

TYPE: amino acid

STRANDEDNESS: Unknown

TOPOLOGY: Unknown

MOLECULE TYPE: Peptide

US-08-417-174-91

Query Match 34.7%; Score 25; DB 1; Length 9;

Best Local Similarity 100.0%; Pred. No. 5e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFSV 5

Db 5 VPFSV 9

RESULT 41

US-08-417-174-92

Sequence 92, Application US/08417174

Patent No. 5844075

GENERAL INFORMATION:

APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,

APPLICANT: STEVEN A.

TITLE OF INVENTION: MELANOMA ANTIGENS AND

TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC

NUMBER OF SEQUENCES: 126

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/417,174

FILING DATE: 05-APR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/231,565

FILING DATE: 22-APR-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-417-174-92

Query Match 34.7%; Score 25; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VFPSV 5
|||
Db 5 VFPSV 9

RESULT 42
US-08-417-174-93
Sequence 93, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & PINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-417-174-93

Query Match 34.7%; Score 25; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VFPSV 5
|||
Db 5 VFPSV 9

RESULT 43
US-08-417-174-94
Sequence 94, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & PINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-417-174-94

Query Match 34.7%; Score 25; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VFPSV 5
|||
Db 5 VFPSV 9

RESULT 44
US-08-417-174-95
Sequence 95, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND

;; TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
;; NUMBER OF SEQUENCES: 126
;; CORRESPONDENCE ADDRESS: 126
;; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
;; STREET: 345 PARK AVENUE
;; CITY: NEW YORK
;; STATE: NEW YORK
;; COUNTRY: USA
;; ZIP: 10154
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: FLOPPY DISK
;; COMPUTER: IBM PC COMPATIBLE
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: ASCII
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/417,174
;; FILING DATE: 05-APR-1995
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: US/08/231,565
;; FILING DATE: 22-APR-1994
;; CLASSIFICATION: 435
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: CAROL M. GRUPPI
;; REGISTRATION NUMBER: 37,341
;; REFERENCE/DOCKET NUMBER: 2026-4124US1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 758-4800
;; TELEFAX: (212) 751-6849
;; TELEX: 421792
;;
;; INFORMATION FOR SEQ ID NO: 95:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9
;; TYPE: amino acid
;; STRANDEDNESS: Unknown
;; TOPOLOGY: Unknown
;; MOLECULE TYPE: Peptide
;;
US-08-417-174-95

Query Match 34.7%; Score 25; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFSV 5
|||
Db 5 VPFSV 9

RESULT 45
US-08-417-174-96
;; Sequence 96, Application US/08417174
;; Patent No. 5844075
;;
;; GENERAL INFORMATION:
;; APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
;; APPLICANT: STEVEN A.
;; TITLE OF INVENTION: MELANOMA ANTIGENS AND
;; TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
;; TITLE OF INVENTION: METHODS
;; NUMBER OF SEQUENCES: 126
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
;; STREET: 345 PARK AVENUE
;; CITY: NEW YORK
;; STATE: NEW YORK
;; COUNTRY: USA
;; ZIP: 10154
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: FLOPPY DISK
;; COMPUTER: IBM PC COMPATIBLE
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: ASCII
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/417,174

;; FILING DATE: 05-APR-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/231,565
;; FILING DATE: 22-APR-1994
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: CAROL M. GRUPPI
;; REGISTRATION NUMBER: 37,341
;; REFERENCE/DOCKET NUMBER: 2026-4124US1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 758-4800
;; TELEFAX: (212) 751-6849
;; TELEX: 421792
;;
;; INFORMATION FOR SEQ ID NO: 96:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9
;; TYPE: amino acid
;; STRANDEDNESS: Unknown
;; TOPOLOGY: Unknown
;; MOLECULE TYPE: Peptide
;;
US-08-417-174-96

Query Match 34.7%; Score 25; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFSV 5
|||
Db 5 VPFSV 9

RESULT 46
US-08-417-174-97
;; Sequence 97, Application US/08417174
;; Patent No. 5844075
;;
;; GENERAL INFORMATION:
;; APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
;; APPLICANT: STEVEN A.
;; TITLE OF INVENTION: MELANOMA ANTIGENS AND
;; TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
;; TITLE OF INVENTION: METHODS
;; NUMBER OF SEQUENCES: 126
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
;; STREET: 345 PARK AVENUE
;; CITY: NEW YORK
;; STATE: NEW YORK
;; COUNTRY: USA
;; ZIP: 10154
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: FLOPPY DISK
;; COMPUTER: IBM PC COMPATIBLE
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: ASCII
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/417,174
;; FILING DATE: 05-APR-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/231,565
;; FILING DATE: 22-APR-1994
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: CAROL M. GRUPPI
;; REGISTRATION NUMBER: 37,341
;; REFERENCE/DOCKET NUMBER: 2026-4124US1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 758-4800
;; TELEFAX: (212) 751-6849
;; TELEX: 421792
;;
;; INFORMATION FOR SEQ ID NO: 97:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9
;; TYPE: amino acid

STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-417-174-97

Query Match 34.7%; Score 25; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSV 5
5 VPFSV 9

Db

RESULT 47
US-08-417-174-98
Sequence 98, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:
APPLICANT: KAMAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELEPHONE: (212) 751-6849
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-417-174-98

Query Match 34.7%; Score 25; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSV 5
5 VPFSV 9

Db

RESULT 48
US-08-417-174-99
Sequence 99, Application US/08417174

Patent No. 5844075
GENERAL INFORMATION:
APPLICANT: KAMAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELEPHONE: (212) 751-6849
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-417-174-99

Query Match 34.7%; Score 25; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSV 5
5 VPFSV 9

Db

RESULT 49
US-08-417-174-100
Sequence 100, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:
APPLICANT: KAMAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-417-174-100

Query Match 34.7%; Score 25; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSV 5
Db 5 VPFSV 9

RESULT 50
US-08-417-174-101
Sequence 101, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA, ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849

TELEX: 421792
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-417-174-101

Query Match 34.7%; Score 25; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSV 5
Db 5 VPFSV 9

RESULT 51
US-08-417-174-102
Sequence 102, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA, ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-417-174-102

Query Match 34.7%; Score 25; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSV 5
Db 5 VPFSV 9

RESULT 52
US-08-417-174-103
; Sequence 103, Application US/08411714
; Patent No. 5844075
; GENERAL INFORMATION:
; APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
; APPLICANT: STEVEN A.
; TITLE OF INVENTION: MELANOMA ANTIGENS AND
; TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 126
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/417,174
; FILING DATE: 05-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/231,565
; FILING DATE: 22-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CAROL M. GRUPPI
; REGISTRATION NUMBER: 37,341
; REFERENCE/DOCKET NUMBER: 2026-4124US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 103:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9
; TYPE: amino acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-417-174-103
Query Match 34.7%; Score 25; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPFSV 5
Db 5 VPFSV 9
RESULT 53
US-08-902-516-30
; Sequence 30, Application US/08902516
; Patent No. 5891432
; GENERAL INFORMATION:
; APPLICANT: Soo Hoo, William
; TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS
; TITLE OF INVENTION: COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE
; TITLE OF INVENTION: RESPONSE USING SAME
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL & FLORES, LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California

COUNTRY: United States
ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/902,516
; FILING DATE: 28-JUL-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-1M 2442
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)535-9001
; TELEFAX: (619)535-8949
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-902-516-30

Query Match 34.7%; Score 25; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSV 5
Db 5 VPFSV 9

RESULT 54
US-09-036-582-27
; Sequence 27, Application US/09036582A
; Patent No. 5965381
; GENERAL INFORMATION:
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Cornelis, Guy R.
; TITLE OF INVENTION: DELIVERY OF PROTEINS INTO EUKARYOTIC CELLS
; TITLE OF INVENTION: WITH RECOMBINANT VERNISINIA
; FILE REFERENCE: 11154
; CURRENT APPLICATION NUMBER: US/09/036,582A
; CURRENT FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human gp100Pmel117 peptide
US-09-036-582-27

Query Match 34.7%; Score 25; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSV 5
Db 5 VPFSV 9

RESULT 55
US-09-183-706-31
; Sequence 31, Application US/09183706
; Patent No. 6245525
; GENERAL INFORMATION:
; APPLICANT: Marcelange, Valrie
; APPLICANT: De Smet, Charles
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR

FILE REFERENCE: L0461/7054
CURRENT APPLICATION NUMBER: US/09/183,706
CURRENT FILING DATE: 1998-10-30
EARLIER APPLICATION NUMBER: 09/122,989
EARLIER FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 43
SEQ ID NO 31
LENGTH: 9
TYPE: PR1
ORGANISM: Homo sapiens
US-09-183-706-31

Query Match 34.7%; Score 25; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPSV 5
Db 5 VPSV 9

RESULT 56
US-09-267-439-48
Sequence 48, Application US/09267439
Patent No. 6270778
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-09-267-439-48

Query Match 34.7%; Score 25; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPSV 5
Db 5 VPSV 9

RESULT 57
US-09-267-439-83
Sequence 83, Application US/09267439
Patent No. 6270778
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-09-267-439-83

Query Match 34.7%; Score 25; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPSV 5
Db 5 VPSV 9

RESULT 58
US-09-267-439-84
Sequence 84, Application US/09267439
Patent No. 6270778
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 126

Query Match 34.7%; Score 25; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
;; STREET: 345 PARK AVENUE
;; CITY: NEW YORK
;; STATE: NEW YORK
;; COUNTRY: USA
;; ZIP: 10154
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: FLOPPY DISK
;; COMPUTER: IBM PC COMPATIBLE
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: ASCII
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/267,439
;; FILING DATE:
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: US/08/417,174
;; FILING DATE: 05-APR-1995
;; APPLICATION NUMBER: US/08/231,565
;; FILING DATE: 22-APR-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: CAROL M. GRUPPI
;; REGISTRATION NUMBER: 37,341
;; REFERENCE/DOCKET NUMBER: 2026-4124US1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 758-4800
;; TELEFAX: (212) 751-6849
;; TELEX: 421792
;; INFORMATION FOR SEQ ID NO: 84:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9
;; TYPE: amino acid
;; STRANDEDNESS: Unknown
;; TOPOLOGY: Unknown
;; MOLECULE TYPE: Peptide
;; US-09-267-439-84

Query Match 34.7%; Score 25; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. Se+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPPSV 5
Db 5 VPPSV 9

RESULT 59
US-09-267-439-85
;; Sequence 85, Application US/09267439
;; Patent No. 6270778
;; GENERAL INFORMATION:
;; APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
;; APPLICANT: STEVEN A.
;; TITLE OF INVENTION: MELANOMA ANTIGENS AND
;; TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
;; TITLE OF INVENTION: METHODS
;; NUMBER OF SEQUENCES: 126
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
;; STREET: 345 PARK AVENUE
;; CITY: NEW YORK
;; STATE: NEW YORK
;; COUNTRY: USA
;; ZIP: 10154
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: FLOPPY DISK
;; COMPUTER: IBM PC COMPATIBLE
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: ASCII
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/267,439
;; FILING DATE:
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: US/09/267,439

;; APPLICATION NUMBER: US/08/417,174
;; FILING DATE: 05-APR-1995
;; APPLICATION NUMBER: US/08/231,565
;; FILING DATE: 22-APR-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: CAROL M. GRUPPI
;; REGISTRATION NUMBER: 37,341
;; REFERENCE/DOCKET NUMBER: 2026-4124US1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 758-4800
;; TELEFAX: (212) 751-6849
;; TELEX: 421792
;; INFORMATION FOR SEQ ID NO: 85:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9
;; TYPE: amino acid
;; STRANDEDNESS: Unknown
;; TOPOLOGY: Unknown
;; MOLECULE TYPE: Peptide
;; US-09-267-439-85

Query Match 34.7%; Score 25; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. Se+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPPSV 5
Db 5 VPPSV 9

RESULT 60
US-09-267-439-86
;; Sequence 86, Application US/09267439
;; Patent No. 6270778
;; GENERAL INFORMATION:
;; APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
;; APPLICANT: STEVEN A.
;; TITLE OF INVENTION: MELANOMA ANTIGENS AND
;; TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
;; TITLE OF INVENTION: METHODS
;; NUMBER OF SEQUENCES: 126
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
;; STREET: 345 PARK AVENUE
;; CITY: NEW YORK
;; STATE: NEW YORK
;; COUNTRY: USA
;; ZIP: 10154
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: FLOPPY DISK
;; COMPUTER: IBM PC COMPATIBLE
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: ASCII
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/267,439
;; FILING DATE:
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: US/08/417,174
;; FILING DATE: 05-APR-1995
;; APPLICATION NUMBER: US/08/231,565
;; FILING DATE: 22-APR-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: CAROL M. GRUPPI
;; REGISTRATION NUMBER: 37,341
;; REFERENCE/DOCKET NUMBER: 2026-4124US1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 758-4800
;; TELEFAX: (212) 751-6849
;; TELEX: 421792
;; INFORMATION FOR SEQ ID NO: 86:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9
;; TYPE: amino acid

STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-09-267-439-86

Query Match 34.7%; Score 25; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSV 5
Db 5 VPFSV 9

RESULT 61
US-09-267-439-87
Sequence 87, Application US/09267439
Patent No. 6270778

GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
NUMBER OF INVENTION: METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-09-267-439-87

Query Match 34.7%; Score 25; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSV 5
Db 5 VPFSV 9

RESULT 62
US-09-267-439-88

Sequence 88, Application US/09267439
Patent No. 6270778
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
NUMBER OF INVENTION: METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-09-267-439-88

Query Match 34.7%; Score 25; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSV 5
Db 5 VPFSV 9

RESULT 63
US-09-267-439-89
Sequence 89, Application US/09267439
Patent No. 6270778
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
NUMBER OF INVENTION: METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 751-6849
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-09-267-439-89

Query Match 34.7%; Score 25; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPPSV 5
|||
Db 5 VPPSV 9

RESULT 64
US-09-267-439-90
Sequence 90, Application US/09267439
Patent No. 6270778
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341

REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 90:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-09-267-439-90

Query Match 34.7%; Score 25; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPPSV 5
|||
Db 5 VPPSV 9

RESULT 65
US-09-267-439-91
Sequence 91, Application US/09267439
Patent No. 6270778
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-09-267-439-91

Query Match 34.7%; Score 25; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPPSV 5

Db 5 VPPSV 9

RESULT 66
US-09-267-439-92

Sequence 92, Application US/09267439

Patent No. 6270778

GENERAL INFORMATION:

APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,

APPLICANT: STEVEN A.

TITLE OF INVENTION: MELANOMA ANTIGENS AND

TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC

TITLE OF INVENTION: METHODS

NUMBER OF SEQUENCES: 126

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/267,439

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/417,174

FILING DATE: 05-APR-1995

APPLICATION NUMBER: US/08/231,565

FILING DATE: 22-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: CAROL M. GRUPPI

REGISTRATION NUMBER: 37,341

REFERENCE/DOCKET NUMBER: 2026-4124US1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 758-4800

TELEFAX: (212) 751-6849

TELEX: 421792

INFORMATION FOR SEQ ID NO: 92:

SEQUENCE CHARACTERISTICS:

LENGTH: 9

TYPE: amino acid

STRANDEDNESS: Unknown

TOPOLOGY: Unknown

MOLECULE TYPE: Peptide

US-09-267-439-92

Query Match

Best local Similarity 34.7%; Score 25; DB 2; Length 9;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPPSV 5

Db 5 VPPSV 9

RESULT 67

US-09-267-439-93

Sequence 93, Application US/09267439

Patent No. 6270778

GENERAL INFORMATION:

APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,

APPLICANT: STEVEN A.

TITLE OF INVENTION: MELANOMA ANTIGENS AND

TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC

TITLE OF INVENTION: METHODS

NUMBER OF SEQUENCES: 126

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/267,439

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/417,174

FILING DATE: 05-APR-1995

APPLICATION NUMBER: US/08/231,565

FILING DATE: 22-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: CAROL M. GRUPPI

REGISTRATION NUMBER: 37,341

REFERENCE/DOCKET NUMBER: 2026-4124US1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 758-4800

TELEFAX: (212) 751-6849

TELEX: 421792

INFORMATION FOR SEQ ID NO: 93:

SEQUENCE CHARACTERISTICS:

LENGTH: 9

TYPE: amino acid

STRANDEDNESS: Unknown

TOPOLOGY: Unknown

MOLECULE TYPE: Peptide

US-09-267-439-93

Query Match

Best local Similarity 34.7%; Score 25; DB 2; Length 9;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPPSV 5

Db 5 VPPSV 9

RESULT 68

US-09-267-439-94

Sequence 94, Application US/09267439

Patent No. 6270778

GENERAL INFORMATION:

APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,

APPLICANT: STEVEN A.

TITLE OF INVENTION: MELANOMA ANTIGENS AND

TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC

TITLE OF INVENTION: METHODS

NUMBER OF SEQUENCES: 126

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/267,439

/ FILING DATE:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/417,174
/ FILING DATE: 05-APR-1995
/ APPLICATION NUMBER: US/08/231,565
/ FILING DATE: 22-APR-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: CAROL M. GRUPPI
/ REGISTRATION NUMBER: 37,341
/ REFERENCE/DOCKET NUMBER: 2026-4124US1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 758-4800
/ TELEFAX: (212) 751-6849
/ TELEEX: 421792
/ INFORMATION FOR SEQ ID NO: 94:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 9
/ TYPE: amino acid
/ STRANDEDNESS: Unknown
/ TOPOLOGY: Unknown
/ MOLECULE TYPE: Peptide
US-09-267-439-94

Query Match 34.7% Score 25; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFSV 5
Db 5 VPFSV 9

RESULT 69
US-09-267-439-95
/ Sequence 95, Application US/09267439
/ Patent No. 6270778
/ GENERAL INFORMATION:
/ APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
/ APPLICANT: STEVEN A.
/ TITLE OF INVENTION: MELANOMA ANTIGENS AND
/ TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
/ TITLE OF INVENTION: METHODS
/ NUMBER OF SEQUENCES: 126
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: MORGAN & PINNEGAN, L.L.P.
/ STREET: 345 PARK AVENUE
/ CITY: NEW YORK
/ STATE: NEW YORK
/ COUNTRY: USA
/ ZIP: 10154
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: FLOPPY DISK
/ COMPUTER: IBM PC COMPATIBLE
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: ASCII
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/267,439
/ FILING DATE:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/417,174
/ FILING DATE: 05-APR-1995
/ APPLICATION NUMBER: US/08/231,565
/ FILING DATE: 22-APR-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: CAROL M. GRUPPI
/ REGISTRATION NUMBER: 37,341
/ REFERENCE/DOCKET NUMBER: 2026-4124US1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 758-4800
/ TELEFAX: (212) 751-6849
/ TELEEX: 421792
/ INFORMATION FOR SEQ ID NO: 95:
/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 9
/ TYPE: amino acid
/ STRANDEDNESS: Unknown
/ TOPOLOGY: Unknown
/ MOLECULE TYPE: Peptide
US-09-267-439-95

Query Match 34.7% Score 25; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFSV 5
Db 5 VPFSV 9

RESULT 70
US-09-267-439-96
/ Sequence 96, Application US/09267439
/ Patent No. 6270778
/ GENERAL INFORMATION:
/ APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
/ APPLICANT: STEVEN A.
/ TITLE OF INVENTION: MELANOMA ANTIGENS AND
/ TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
/ TITLE OF INVENTION: METHODS
/ NUMBER OF SEQUENCES: 126
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: MORGAN & PINNEGAN, L.L.P.
/ STREET: 345 PARK AVENUE
/ CITY: NEW YORK
/ STATE: NEW YORK
/ COUNTRY: USA
/ ZIP: 10154
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: FLOPPY DISK
/ COMPUTER: IBM PC COMPATIBLE
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: ASCII
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/267,439
/ FILING DATE:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/417,174
/ FILING DATE: 05-APR-1995
/ APPLICATION NUMBER: US/08/231,565
/ FILING DATE: 22-APR-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: CAROL M. GRUPPI
/ REGISTRATION NUMBER: 37,341
/ REFERENCE/DOCKET NUMBER: 2026-4124US1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 758-4800
/ TELEFAX: (212) 751-6849
/ TELEEX: 421792
/ INFORMATION FOR SEQ ID NO: 96:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 9
/ TYPE: amino acid
/ STRANDEDNESS: Unknown
/ TOPOLOGY: Unknown
/ MOLECULE TYPE: Peptide
US-09-267-439-96

Query Match 34.7% Score 25; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFSV 5
Db 5 VPFSV 9

RESULT 71
US-09-267-439-97
Sequence 97, Application US/09267439
Patent No. 6270778
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA, ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & PINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-09-267-439-97
Query Match 34.7%; Score 25; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VPFSV 5
Db 5 VPFSV 9
RESULT 72
US-09-267-439-98
Sequence 98, Application US/09267439
Patent No. 6270778
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA, ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & PINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK

COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-09-267-439-98

Query Match 34.7%; Score 25; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VPFSV 5
Db 5 VPFSV 9

RESULT 73
US-09-267-439-99
Sequence 99, Application US/09267439
Patent No. 6270778
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA, ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & PINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:

NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-09-267-439-99

Query Match 34.7%; Score 25; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFSV 5
Db 5 VPFSV 9

RESULT 74
US-09-267-439-100
Sequence 100, Application US/09267439
Patent No. 6270778
GENERAL INFORMATION:
APPLICANT: KAMAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-09-267-439-100

Query Match 34.7%; Score 25; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFSV 5
Db 5 VPFSV 9

RESULT 75
US-09-267-439-101
Sequence 101, Application US/09267439
Patent No. 6270778
GENERAL INFORMATION:
APPLICANT: KAMAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-09-267-439-101

Query Match 34.7%; Score 25; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFSV 5
Db 5 VPFSV 9

RESULT 76
US-09-267-439-102
Sequence 102, Application US/09267439
Patent No. 6270778
GENERAL INFORMATION:
APPLICANT: KAMAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.

TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-09-267-439-102

Query Match 34.7%; Score 25; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSV 5
Db 5 VPFSV 9

RESULT 77
US-09-267-439-103
Sequence 103, Application US/09267439
Patent No. 6270778
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-09-267-439-103

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Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSV 5
Db 5 VPFSV 9

RESULT 78
US-09-166-448-72
Sequence 72, Application US/09166448
Patent No. 6291430
GENERAL INFORMATION:
APPLICANT: Chaux, Pascal
APPLICANT: Vantomme, Valrie
APPLICANT: Strobant, Vincent
APPLICANT: Boon-Falleur, Thierry
APPLICANT: Thielemans, Kris
APPLICANT: Cortals, Jurgen
TITLE OF INVENTION: MAGS-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
FILE REFERENCE: L0461/7052
CURRENT APPLICATION NUMBER: US/09/166,448
CURRENT FILING DATE: 1998-10-05
NUMBER OF SEQ ID NOS: 81
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 72
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-166-448-72

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Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSV 5
Db 5 VPFSV 9

RESULT 79
US-09-567-995-31
Sequence 31, Application US/09567995
Patent No. 6303756
GENERAL INFORMATION:
APPLICANT: Martelange, Val,rie

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/ APPLICANT: De Smet, Charles
/ APPLICANT: Boon-Falleur, Thierry
/ TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR
/ FILE REFERENCE: I0461/7054
/ CURRENT APPLICATION NUMBER: US/09/567,995
/ CURRENT FILING DATE: 2000-05-10
/ PRIOR APPLICATION NUMBER: 09/183,706
/ PRIOR FILING DATE: 1998-10-30
/ NUMBER OF SEQ ID NOS: 43
/ SEQ ID NO 31
/ LENGTH: 9
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/ ORGANISM: Homo sapiens
US-09-567-995-31
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Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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/ Sequence 5, Application US/09249272
/ Patent No. 6306640
/ GENERAL INFORMATION:
/ APPLICANT: Nicolette, Charles
/ TITLE OF INVENTION: MELANOMA ANTIGENIC PEPTIDES
/ FILE REFERENCE: GA015205
/ CURRENT APPLICATION NUMBER: US/09/249,272
/ CURRENT FILING DATE: 1999-02-11
/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 5
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (1..7)
/ OTHER INFORMATION: Natural epitope, melanoma antigen gp100 aas 209-217
US-09-249-272-5
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Query Match          34.7%; Score 25; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      5 VPFSV 9
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Search completed: July 12, 2006, 05:40:40
Job time : 57 secs
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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 12, 2006, 05:51:14 ; Search time 27 Seconds
(without alignments)
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Title: US-10-671-019-2

Perfect score: 72

Sequence: 1 VPFSAKSVKSLYLIG 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 204771 seqs, 57208143 residues

Total number of hits satisfying chosen parameters: 21003

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Maximum Match 0%

Maximum Match 100%
Listing first 800 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	23	31.9	11	6	US-10-538-066-370	Sequence 370, Appl
6	23	31.9	12	7	US-10-522-086-21	Sequence 21, Appl
7	23	31.9	12	7	US-11-298-560-36	Sequence 36, Appl
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9	22	30.6	12	7	US-11-122-986-469	Sequence 469, Appl
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148	18	25.0	12	6	US-10-953-613C-111	Sequence 111, App	221	17	23.6	17	7	US-11-061-841-308	Sequence 308, App
149	18	25.0	12	6	US-10-953-613C-112	Sequence 112, App	222	17	23.6	17	7	US-11-061-841-309	Sequence 309, App
150	18	25.0	12	6	US-10-953-613C-113	Sequence 113, App	223	17	23.6	17	7	US-11-061-841-311	Sequence 311, App
151	18	25.0	12	6	US-10-953-613C-116	Sequence 116, App	224	17	23.6	17	7	US-11-061-841-312	Sequence 312, App
152	18	25.0	12	6	US-10-953-613C-118	Sequence 118, App	225	17	23.6	17	7	US-11-061-841-313	Sequence 313, App
153	18	25.0	12	6	US-10-953-613C-121	Sequence 121, App	226	17	23.6	17	7	US-11-061-841-314	Sequence 314, App
154	18	25.0	12	6	US-10-953-613C-124	Sequence 124, App	227	17	23.6	17	7	US-11-259-133-87	Sequence 87, Appl
155	18	25.0	12	6	US-10-953-613C-125	Sequence 125, App	228	17	23.6	17	7	US-11-259-266-15	Sequence 15, Appl
156	18	25.0	12	6	US-10-953-613C-126	Sequence 126, App	229	17	23.6	17	7	US-11-259-267-15	Sequence 15, Appl
157	18	25.0	12	6	US-10-953-613C-132	Sequence 132, App	230	17	23.6	17	7	US-11-247-376-17	Sequence 17, Appl
158	18	25.0	12	6	US-10-953-613C-134	Sequence 134, App	231	17	23.6	17	7	US-11-303-372-99	Sequence 99, Appl
159	18	25.0	12	6	US-10-953-613C-136	Sequence 136, App	232	17	23.6	17	7	US-10-538-066-439	Sequence 439, App
160	18	25.0	12	6	US-10-953-613C-146	Sequence 146, App	233	17	23.6	17	7	US-10-536-804-46	Sequence 46, Appl
161	18	25.0	12	6	US-10-953-613C-152	Sequence 152, App	234	17	23.6	9	6	US-10-781-841-75	Sequence 75, Appl
162	18	25.0	12	6	US-10-953-613C-155	Sequence 155, App	235	17	23.6	9	7	US-11-247-376-12	Sequence 12, Appl
163	18	25.0	12	6	US-10-953-613C-160	Sequence 160, App	236	17	23.6	9	7	US-11-247-376-13	Sequence 13, Appl
164	18	25.0	12	6	US-10-953-613C-164	Sequence 164, App	237	17	23.6	9	7	US-11-247-376-14	Sequence 14, Appl
165	18	25.0	12	6	US-10-953-613C-218	Sequence 218, App	238	17	23.6	9	7	US-11-247-376-15	Sequence 15, Appl
166	18	25.0	12	6	US-10-953-613C-219	Sequence 219, App	239	17	23.6	9	7	US-11-247-376-16	Sequence 16, Appl
167	18	25.0	12	6	US-10-953-613C-219	Sequence 219, App	240	17	23.6	9	7	US-11-140-487A-214	Sequence 214, App
168	18	25.0	12	6	US-10-953-613C-392	Sequence 392, App	241	17	23.6	9	7	US-11-140-487A-1126	Sequence 1126, Ap
169	18	25.0	12	6	US-10-953-613C-412	Sequence 412, App	242	17	23.6	9	7	US-11-140-487A-1429	Sequence 1429, Ap
170	18	25.0	12	7	US-11-122-986-799	Sequence 799, App	243	17	23.6	9	7	US-11-140-487A-1439	Sequence 1439, Ap
171	18	25.0	12	7	US-11-051-725-191	Sequence 191, App	244	17	23.6	9	7	US-11-140-487A-1632	Sequence 1632, Ap

245	17	23.6	9	7	US-11-140-487A-1654	Sequence 1654, Ap	318	17	23.6	15	6	US-10-528-960-18	Sequence 18, App1
246	17	23.6	9	7	US-11-303-372-98	Sequence 98, App1	319	17	23.6	15	7	US-11-247-376-1	Sequence 1, App1
247	17	23.6	9	7	US-11-332-378-130	Sequence 130, App	320	17	23.6	15	7	US-11-247-376-2	Sequence 2, App1
248	17	23.6	9	7	US-11-332-378-140	Sequence 140, App	321	17	23.6	15	7	US-11-247-376-3	Sequence 3, App1
249	17	23.6	9	7	US-11-332-378-205	Sequence 205, App	322	17	23.6	15	7	US-11-247-376-4	Sequence 4, App1
250	17	23.6	9	7	US-11-340-431-95	Sequence 95, App1	323	17	23.6	15	7	US-11-247-376-5	Sequence 5, App1
251	17	23.6	9	7	US-11-340-431-123	Sequence 123, App	324	17	23.6	15	7	US-11-247-376-7	Sequence 7, App1
252	17	23.6	9	7	US-11-340-431-129	Sequence 129, App	325	17	23.6	15	7	US-11-247-376-8	Sequence 8, App1
253	17	23.6	9	7	US-11-340-431-207	Sequence 207, App	326	17	23.6	15	7	US-11-247-376-9	Sequence 9, App1
254	17	23.6	9	7	US-11-340-431-232	Sequence 234, App	327	17	23.6	15	7	US-11-247-376-10	Sequence 10, App1
255	17	23.6	9	7	US-11-340-431-277	Sequence 277, App	328	17	23.6	15	7	US-11-247-376-11	Sequence 11, App1
256	17	23.6	9	7	US-11-194-879-27	Sequence 27, App1	329	17	23.6	15	7	US-11-247-376-19	Sequence 19, App1
257	17	23.6	9	7	US-11-253-240-6	Sequence 6, App1	330	17	23.6	15	7	US-11-247-376-20	Sequence 20, App1
258	17	23.6	9	7	US-11-099-2838-463	Sequence 463, App	331	17	23.6	15	7	US-11-247-376-21	Sequence 21, App1
259	17	23.6	10	6	US-10-474-853-26	Sequence 26, App1	332	17	23.6	15	7	US-11-247-376-22	Sequence 22, App1
260	17	23.6	10	6	US-10-486-845A-1	Sequence 1, App1	333	17	23.6	15	7	US-11-247-376-24	Sequence 24, App1
261	17	23.6	10	6	US-10-538-066-240	Sequence 240, App	334	17	23.6	15	7	US-11-247-376-25	Sequence 25, App1
262	17	23.6	10	6	US-10-538-066-524	Sequence 524, App	335	17	23.6	15	7	US-11-140-487A-2208	Sequence 2208, Ap
263	17	23.6	10	6	US-10-648-139A-21	Sequence 21, App1	336	17	23.6	15	7	US-11-295-192A-167	Sequence 167, App
264	17	23.6	10	7	US-11-140-487A-1052	Sequence 1052, Ap	337	17	23.6	15	7	US-11-295-192A-168	Sequence 168, App
265	17	23.6	10	7	US-11-140-487A-1127	Sequence 1127, Ap	338	17	23.6	15	7	US-11-295-192A-169	Sequence 169, App
266	17	23.6	10	7	US-11-140-487A-1440	Sequence 1440, Ap	339	17	23.6	15	7	US-11-295-192A-170	Sequence 170, App
267	17	23.6	10	7	US-11-303-372-90	Sequence 90, App1	340	17	23.6	15	7	US-11-295-192A-171	Sequence 171, App
268	17	23.6	10	7	US-11-122-986-201	Sequence 201, App	341	17	23.6	15	7	US-11-295-192A-172	Sequence 172, App
269	17	23.6	10	7	US-11-061-841-106	Sequence 106, App	342	17	23.6	15	7	US-11-295-192A-173	Sequence 173, App
270	17	23.6	10	7	US-11-061-841-107	Sequence 107, App	343	17	23.6	15	7	US-11-295-192A-174	Sequence 174, App
271	17	23.6	10	7	US-11-061-841-108	Sequence 108, App	344	17	23.6	15	7	US-11-295-192A-175	Sequence 175, App
272	17	23.6	10	7	US-11-061-841-109	Sequence 109, App	345	17	23.6	15	7	US-11-295-192A-176	Sequence 176, App
273	17	23.6	10	7	US-11-061-841-110	Sequence 110, App	346	17	23.6	15	7	US-11-295-192A-177	Sequence 177, App
274	17	23.6	10	7	US-11-061-841-111	Sequence 111, App	347	17	23.6	15	7	US-11-295-192A-225	Sequence 225, App
275	17	23.6	10	7	US-11-061-841-114	Sequence 114, App	348	17	23.6	15	7	US-11-295-192A-226	Sequence 226, App
276	17	23.6	10	7	US-11-061-841-116	Sequence 116, App	349	17	23.6	15	7	US-11-295-192A-237	Sequence 237, App
277	17	23.6	10	7	US-11-061-841-117	Sequence 117, App	350	17	23.6	15	7	US-11-295-192A-238	Sequence 238, App
278	17	23.6	10	7	US-11-061-841-120	Sequence 120, App	351	17	23.6	15	7	US-11-295-192A-229	Sequence 229, App
279	17	23.6	10	7	US-11-061-841-123	Sequence 123, App	352	17	23.6	15	7	US-11-295-192A-230	Sequence 230, App
280	17	23.6	10	7	US-11-061-841-124	Sequence 124, App	353	17	23.6	15	7	US-11-295-192A-306	Sequence 306, App
281	17	23.6	10	7	US-11-061-841-125	Sequence 125, App	354	17	23.6	15	7	US-11-295-192A-307	Sequence 307, App
282	17	23.6	10	7	US-11-293-891-3	Sequence 3, App1	355	17	23.6	15	7	US-11-295-192A-308	Sequence 308, App
283	17	23.6	10	7	US-11-099-2838-497	Sequence 497, App	356	17	23.6	15	7	US-11-295-192A-309	Sequence 309, App
284	17	23.6	10	7	US-11-327-214-6	Sequence 6, App1	357	17	23.6	15	7	US-11-295-192A-310	Sequence 310, App
285	17	23.6	11	6	US-10-525-126-3	Sequence 3, App1	358	17	23.6	15	7	US-11-295-192A-311	Sequence 311, App
286	17	23.6	11	6	US-10-538-066-470	Sequence 470, App	359	17	23.6	15	7	US-11-295-192A-312	Sequence 312, App
287	17	23.6	11	7	US-11-219-121-7	Sequence 7, App1	360	17	23.6	15	7	US-11-295-192A-313	Sequence 313, App
288	17	23.6	11	7	US-11-303-372-89	Sequence 89, App1	361	17	23.6	15	7	US-11-295-192A-314	Sequence 314, App
289	17	23.6	11	7	US-11-303-372-96	Sequence 96, App1	362	17	23.6	15	7	US-11-295-192A-315	Sequence 315, App
290	17	23.6	11	7	US-11-303-372-100	Sequence 100, App	363	17	23.6	15	7	US-11-295-192A-316	Sequence 316, App
291	17	23.6	12	6	US-10-531-701-1	Sequence 1, App1	364	17	23.6	15	7	US-11-295-192A-317	Sequence 317, App
292	17	23.6	12	6	US-10-953-613C-115	Sequence 115, App	365	17	23.6	15	7	US-11-295-192A-474	Sequence 474, App
293	17	23.6	12	6	US-10-953-613C-120	Sequence 120, App	366	17	23.6	15	7	US-11-295-192A-487	Sequence 487, App
294	17	23.6	12	6	US-10-953-613C-216	Sequence 216, App	367	17	23.6	15	7	US-11-295-192A-895	Sequence 895, App
295	17	23.6	12	6	US-10-953-613C-230	Sequence 230, App	368	17	23.6	15	7	US-11-295-192A-1238	Sequence 1238, App
296	17	23.6	12	6	US-10-953-613C-193	Sequence 193, App	369	17	23.6	15	7	US-11-295-192A-1239	Sequence 1239, App
297	17	23.6	12	7	US-11-176-182-115	Sequence 115, App	370	17	23.6	15	7	US-11-295-192A-1240	Sequence 1240, App
298	17	23.6	12	7	US-11-303-372-95	Sequence 95, App1	371	17	23.6	15	7	US-11-134-871-833	Sequence 833, App
299	17	23.6	12	7	US-11-303-372-97	Sequence 97, App1	372	17	23.6	15	7	US-11-134-871-833	Sequence 833, App
300	17	23.6	12	7	US-11-305-401-1	Sequence 1, App1	373	17	23.6	15	7	US-11-134-871-3271	Sequence 3271, App
301	17	23.6	13	6	US-10-531-701-29	Sequence 29, App1	374	17	23.6	15	7	US-11-134-871-3475	Sequence 3475, App
302	17	23.6	13	7	US-11-303-372-87	Sequence 87, App1	375	17	23.6	15	7	US-11-134-871-3536	Sequence 3536, App
303	17	23.6	13	7	US-11-303-372-91	Sequence 91, App1	376	17	23.6	15	7	US-11-134-871-3475	Sequence 3475, App
304	17	23.6	13	7	US-11-061-841-381	Sequence 381, App	377	17	23.6	15	7	US-11-263-230-1429	Sequence 1429, App
305	17	23.6	13	7	US-11-354-653-106	Sequence 106, App	378	17	23.6	15	7	US-11-263-230-1430	Sequence 1430, App
306	17	23.6	13	7	US-11-366-001-125	Sequence 125, App	379	17	23.6	15	7	US-11-263-230-1431	Sequence 1431, App
307	17	23.6	13	7	US-11-366-001-126	Sequence 126, App	380	17	23.6	15	7	US-11-263-230-1432	Sequence 1432, App
308	17	23.6	14	6	US-09-731-899-25	Sequence 25, App1	381	17	23.6	15	7	US-11-263-230-1426	Sequence 1426, App
309	17	23.6	14	6	US-10-489-071-1	Sequence 1, App1	382	17	23.6	15	7	US-11-263-230-1427	Sequence 1427, App
310	17	23.6	14	6	US-10-489-071-2	Sequence 2, App1	383	17	23.6	15	7	US-11-263-230-1428	Sequence 1428, App
311	17	23.6	14	6	US-10-449-902-29189	Sequence 29189, A	384	17	23.6	15	7	US-11-263-230-1429	Sequence 1429, App
312	17	23.6	14	7	US-11-272-521-31	Sequence 31, App1	385	17	23.6	15	7	US-11-263-230-1430	Sequence 1430, App
313	17	23.6	14	7	US-11-134-871-1295	Sequence 1295, App	386	17	23.6	15	7	US-11-263-230-1431	Sequence 1431, App
314	17	23.6	14	7	US-11-134-871-1295	Sequence 1295, App	387	17	23.6	15	7	US-11-263-230-1432	Sequence 1432, App
315	17	23.6	14	7	US-11-234-731-512	Sequence 2286, App	388	17	23.6	15	7	US-11-140-487A-1283	Sequence 1283, App
316	17	23.6	14	7	US-11-242-617-35	Sequence 35, App1	389	17	23.6	15	7	US-11-122-986-830	Sequence 830, App
317	17	23.6	14	7	US-11-261-451-9	Sequence 9, App1	390	17	23.6	15	7	US-11-178-155-29	Sequence 29, App1

331	16	22.2	8	7	US-11-294-621-510	Sequence 510, App	464	16	22.2	12	7	US-11-140-487A-2260	Sequence 2260, Ap
332	16	22.2	9	6	US-10-538-066-142	Sequence 142, App	465	16	22.2	12	7	US-11-142-051-18	Sequence 18, App1
333	16	22.2	9	6	US-10-538-066-340	Sequence 340, App	466	16	22.2	12	7	US-11-305-657-4	Sequence 4, App1
334	16	22.2	9	6	US-10-538-066-749	Sequence 749, App	467	16	22.2	12	7	US-11-178-155-42	Sequence 42, App1
335	16	22.2	9	6	US-10-620-289-19	Sequence 19, App1	468	16	22.2	12	7	US-11-247-659-3	Sequence 3, App1
336	16	22.2	9	6	US-10-536-804-49	Sequence 49, App1	469	16	22.2	12	7	US-11-281-266-70	Sequence 70, App1
337	16	22.2	9	7	US-11-140-487A-8	Sequence 8, App1	470	16	22.2	12	7	US-11-313-104-8	Sequence 8, App1
338	16	22.2	9	7	US-11-140-487A-20	Sequence 20, App1	471	16	22.2	13	6	US-10-538-066-39	Sequence 10, App1
339	16	22.2	9	7	US-11-140-487A-212	Sequence 212, App	472	16	22.2	13	6	US-10-538-066-63	Sequence 39, App1
400	16	22.2	9	7	US-11-140-487A-358	Sequence 358, App	473	16	22.2	13	6	US-10-538-066-69	Sequence 69, App1
401	16	22.2	9	7	US-11-140-487A-417	Sequence 417, App	474	16	22.2	13	7	US-11-038-754-18	Sequence 18, App1
422	16	22.2	9	7	US-11-140-487A-443	Sequence 443, App	475	16	22.2	13	7	US-11-261-429-30	Sequence 30, App1
403	16	22.2	9	7	US-11-140-487A-472	Sequence 472, App	476	16	22.2	13	7	US-11-061-841-375	Sequence 375, App1
404	16	22.2	9	7	US-11-140-487A-510	Sequence 510, App	477	16	22.2	13	7	US-11-134-871-1328	Sequence 1328, App
405	16	22.2	9	7	US-11-140-487A-518	Sequence 518, App	478	16	22.2	13	7	US-11-134-871-3328	Sequence 3328, Ap
406	16	22.2	9	7	US-11-140-487A-524	Sequence 524, App	479	16	22.2	13	7	US-11-134-871-3574	Sequence 3574, Ap
407	16	22.2	9	7	US-11-140-487A-531	Sequence 531, App	480	16	22.2	13	7	US-11-134-871-3594	Sequence 3594, Ap
408	16	22.2	9	7	US-11-140-487A-680	Sequence 680, App	481	16	22.2	13	7	US-11-368-086-117	Sequence 117, App1
409	16	22.2	9	7	US-11-140-487A-684	Sequence 684, App	482	16	22.2	14	6	US-10-499-266-17	Sequence 17, App1
410	16	22.2	9	7	US-11-140-487A-747	Sequence 747, App	483	16	22.2	14	7	US-11-122-986-361	Sequence 361, App1
411	16	22.2	9	7	US-11-140-487A-875	Sequence 875, App	484	16	22.2	14	7	US-11-257-818-55	Sequence 55, App1
412	16	22.2	9	7	US-11-140-487A-888	Sequence 888, App	485	16	22.2	14	7	US-11-134-871-989	Sequence 989, App
413	16	22.2	9	7	US-11-140-487A-1116	Sequence 1116, App	486	16	22.2	14	7	US-11-134-871-3158	Sequence 3158, App
414	16	22.2	9	7	US-11-140-487A-1118	Sequence 1118, App	487	16	22.2	15	6	US-10-901-423-10	Sequence 10, App1
415	16	22.2	9	7	US-11-140-487A-1124	Sequence 1124, App	488	16	22.2	15	7	US-11-140-487A-2102	Sequence 2102, Ap
416	16	22.2	9	7	US-11-140-487A-1144	Sequence 1144, App	489	16	22.2	15	7	US-11-140-487A-2129	Sequence 2129, Ap
417	16	22.2	9	7	US-11-140-487A-1185	Sequence 1185, App	490	16	22.2	15	7	US-11-140-487A-2140	Sequence 2140, Ap
418	16	22.2	9	7	US-11-140-487A-1351	Sequence 1351, App	491	16	22.2	15	7	US-11-140-487A-2148	Sequence 2148, Ap
419	16	22.2	9	7	US-11-140-487A-1476	Sequence 1476, App	492	16	22.2	15	7	US-11-140-487A-2195	Sequence 2195, Ap
420	16	22.2	9	7	US-11-140-487A-1581	Sequence 1581, App	493	16	22.2	15	7	US-11-251-195-3	Sequence 3, App1
421	16	22.2	9	7	US-11-140-487A-1791	Sequence 1791, App	494	16	22.2	15	7	US-11-295-192A-79	Sequence 79, App1
422	16	22.2	9	7	US-11-140-487A-1791	Sequence 1791, App	495	16	22.2	15	7	US-11-295-192A-80	Sequence 80, App1
423	16	22.2	9	7	US-11-155-929-39	Sequence 39, App1	496	16	22.2	15	7	US-11-295-192A-81	Sequence 81, App1
424	16	22.2	9	7	US-11-122-986-526	Sequence 526, App1	497	16	22.2	15	7	US-11-295-192A-82	Sequence 82, App1
425	16	22.2	9	7	US-11-251-195-4	Sequence 4, App1	498	16	22.2	15	7	US-11-295-192A-83	Sequence 83, App1
426	16	22.2	9	7	US-11-099-283B-408	Sequence 408, App	499	16	22.2	15	7	US-11-295-192A-84	Sequence 84, App1
427	16	22.2	10	7	US-11-301-554-2106	Sequence 2106, App	500	16	22.2	15	7	US-11-295-192A-85	Sequence 85, App1
428	16	22.2	10	7	US-11-140-487A-1079	Sequence 1079, App	501	16	22.2	15	7	US-11-295-192A-86	Sequence 86, App1
429	16	22.2	10	7	US-11-140-487A-1112	Sequence 1112, App	502	16	22.2	15	7	US-11-295-192A-87	Sequence 87, App1
430	16	22.2	10	7	US-11-140-487A-1117	Sequence 1117, App	503	16	22.2	15	7	US-11-295-192A-88	Sequence 88, App1
431	16	22.2	10	7	US-11-140-487A-1119	Sequence 1119, App	504	16	22.2	15	7	US-11-295-192A-89	Sequence 89, App1
432	16	22.2	10	7	US-11-140-487A-1125	Sequence 1125, App	505	16	22.2	15	7	US-11-295-192A-90	Sequence 90, App1
433	16	22.2	10	7	US-11-140-487A-1284	Sequence 1284, App	506	16	22.2	15	7	US-11-295-192A-108	Sequence 108, App
434	16	22.2	10	7	US-11-140-487A-1285	Sequence 1285, App	507	16	22.2	15	7	US-11-295-192A-109	Sequence 109, App
435	16	22.2	10	7	US-11-140-487A-1317	Sequence 1317, App	508	16	22.2	15	7	US-11-295-192A-110	Sequence 110, App
436	16	22.2	10	7	US-11-140-487A-1459	Sequence 1459, App	509	16	22.2	15	7	US-11-295-192A-111	Sequence 111, App
437	16	22.2	10	7	US-11-140-487A-1513	Sequence 1513, App	510	16	22.2	15	7	US-11-295-192A-112	Sequence 112, App
438	16	22.2	10	7	US-11-140-487A-1522	Sequence 1522, App	511	16	22.2	15	7	US-11-295-192A-113	Sequence 113, App
439	16	22.2	10	7	US-11-140-487A-1524	Sequence 1524, App	512	16	22.2	15	7	US-11-295-192A-114	Sequence 114, App
440	16	22.2	10	7	US-11-140-487A-1535	Sequence 1535, App	513	16	22.2	15	7	US-11-295-192A-115	Sequence 115, App
441	16	22.2	10	7	US-11-140-487A-1594	Sequence 1594, App	514	16	22.2	15	7	US-11-295-192A-116	Sequence 116, App
442	16	22.2	10	7	US-11-140-487A-1672	Sequence 1672, App	515	16	22.2	15	7	US-11-295-192A-117	Sequence 117, App
443	16	22.2	10	7	US-11-140-487A-1771	Sequence 1771, App	516	16	22.2	15	7	US-11-295-192A-118	Sequence 118, App
444	16	22.2	10	7	US-11-140-487A-1873	Sequence 1873, App	517	16	22.2	15	7	US-11-295-192A-119	Sequence 119, App
445	16	22.2	10	7	US-11-140-487A-1959	Sequence 1959, App	518	16	22.2	15	7	US-11-295-192A-120	Sequence 120, App
446	16	22.2	10	7	US-11-140-487A-1960	Sequence 1960, App	519	16	22.2	15	7	US-11-295-192A-258	Sequence 258, App
447	16	22.2	10	7	US-11-122-986-39	Sequence 39, App1	520	16	22.2	15	7	US-11-295-192A-259	Sequence 259, App
448	16	22.2	10	7	US-11-061-841-115	Sequence 115, App	521	16	22.2	15	7	US-11-295-192A-260	Sequence 260, App
449	16	22.2	11	6	US-11-187-891-23	Sequence 23, App1	522	16	22.2	15	7	US-11-295-192A-261	Sequence 261, App
450	16	22.2	11	6	US-10-538-066-127	Sequence 127, App	523	16	22.2	15	7	US-11-295-192A-262	Sequence 262, App
451	16	22.2	11	6	US-10-538-066-138	Sequence 128, App	524	16	22.2	15	7	US-11-295-192A-263	Sequence 263, App
452	16	22.2	11	6	US-10-538-066-342	Sequence 342, App	525	16	22.2	15	7	US-11-295-192A-264	Sequence 264, App
453	16	22.2	11	6	US-11-122-986-532	Sequence 532, App	526	16	22.2	15	7	US-11-295-192A-265	Sequence 265, App
454	16	22.2	11	7	US-11-061-841-173	Sequence 173, App	527	16	22.2	15	7	US-11-295-192A-266	Sequence 266, App
455	16	22.2	11	7	US-11-061-841-183	Sequence 183, App	528	16	22.2	15	7	US-11-295-192A-728	Sequence 728, App
456	16	22.2	11	7	US-11-253-223-37	Sequence 37, App1	529	16	22.2	15	7	US-11-295-192A-894	Sequence 894, App
457	16	22.2	11	7	US-11-099-283B-192	Sequence 392, App	530	16	22.2	15	7	US-11-134-871-102	Sequence 102, App
458	16	22.2	11	7	US-11-178-155-9	Sequence 9, App1	531	16	22.2	15	7	US-11-134-871-891	Sequence 891, App
459	16	22.2	11	7	US-11-187-891-26	Sequence 26, App1	532	16	22.2	15	7	US-11-134-871-892	Sequence 892, App
460	16	22.2	12	6	US-10-449-902-31392	Sequence 31392, A	533	16	22.2	15	7	US-11-051-725-165	Sequence 165, App
461	16	22.2	12	6	US-10-502-771-36	Sequence 36, App1	534	16	22.2	15	7	US-11-346-079-62	Sequence 62, App1
462	16	22.2	12	6	US-10-953-613C-634	Sequence 633, App	535	16	22.2	15	7	US-11-346-079-63	Sequence 63, App1
463	16	22.2	12	6	US-10-953-613C-635	Sequence 635, App	536	16	22.2	15	7	US-11-346-079-91	Sequence 91, App1

537	16	22.2	15	7	US-11-346-079-118	Sequence 118, App	610	15	20.8	9	7	US-11-155-929-59	Sequence 59, App1
538	15.5	21.5	11	7	US-11-061-841-46	Sequence 46, App1	611	15	20.8	9	7	US-11-155-929-60	Sequence 60, App1
539	15.5	21.5	11	7	US-11-061-841-48	Sequence 48, App1	612	15	20.8	9	7	US-11-155-929-124	Sequence 124, App
540	15.5	21.5	11	7	US-11-061-841-51	Sequence 51, App1	613	15	20.8	9	7	US-11-167-773-80	Sequence 80, App1
541	15.5	21.5	11	7	US-11-061-841-52	Sequence 52, App1	614	15	20.8	9	7	US-11-332-378-41	Sequence 41, App1
542	15.5	21.5	11	7	US-11-061-841-59	Sequence 59, App1	615	15	20.8	9	7	US-11-332-378-166	Sequence 166, App
543	15.5	21.5	11	7	US-11-061-841-61	Sequence 61, App1	616	15	20.8	9	7	US-11-332-378-166	Sequence 1, App1
544	15.5	21.5	11	7	US-11-061-841-62	Sequence 62, App1	617	15	20.8	9	7	US-11-340-431-67	Sequence 67, App1
545	15.5	21.5	11	7	US-11-061-841-65	Sequence 65, App1	618	15	20.8	9	7	US-11-340-431-208	Sequence 208, App
546	15	20.8	5	6	US-10-804-787-1	Sequence 1, App11	619	15	20.8	9	7	US-11-151-999-1	Sequence 1, App11
547	15	20.8	5	6	US-10-524-250-1	Sequence 1, App11	620	15	20.8	9	7	US-11-247-659-2	Sequence 2, App11
548	15	20.8	5	7	US-11-298-344-69	Sequence 69, App1	621	15	20.8	9	7	US-11-286-917-4	Sequence 4, App11
549	15	20.8	5	7	US-11-023-959A-16	Sequence 16, App1	622	15	20.8	9	7	US-11-286-917-24	Sequence 24, App1
550	15	20.8	5	7	US-11-023-959A-70	Sequence 70, App1	623	15	20.8	9	7	US-11-330-822-70	Sequence 70, App1
551	15	20.8	5	7	US-11-257-818-44	Sequence 44, App1	624	15	20.8	10	6	US-10-538-079-74	Sequence 74, App1
552	15	20.8	5	7	US-11-317-846-1	Sequence 1, App11	625	15	20.8	10	6	US-10-538-066-143	Sequence 143, App
553	15	20.8	5	7	US-11-317-814-1	Sequence 1, App11	626	15	20.8	10	6	US-10-538-066-144	Sequence 144, App
554	15	20.8	6	7	US-11-252-376-114	Sequence 114, App	627	15	20.8	10	6	US-10-538-066-692	Sequence 692, App
555	15	20.8	6	7	US-11-257-062-49	Sequence 49, App1	628	15	20.8	10	6	US-10-506-334-18	Sequence 18, App1
556	15	20.8	6	7	US-11-213-668-40	Sequence 40, App1	629	15	20.8	10	6	US-10-648-139A-20	Sequence 20, App1
557	15	20.8	7	1	US-09-784-950-5	Sequence 5, App11	630	15	20.8	10	6	US-10-781-659-4	Sequence 4, App11
558	15	20.8	7	6	US-10-489-071-9	Sequence 9, App11	631	15	20.8	10	6	US-10-781-659-54	Sequence 54, App1
559	15	20.8	7	6	US-10-480-434A-21	Sequence 21, App1	632	15	20.8	10	6	US-10-518-941-17	Sequence 17, App1
560	15	20.8	7	7	US-11-263-230-1213	Sequence 1213, App	633	15	20.8	10	7	US-11-140-487A-795	Sequence 795, App
561	15	20.8	7	7	US-11-263-230-1237	Sequence 1237, App	634	15	20.8	10	7	US-11-140-487A-941	Sequence 941, App
562	15	20.8	7	7	US-11-061-841-299	Sequence 299, App	635	15	20.8	10	7	US-11-140-487A-1001	Sequence 1001, App
563	15	20.8	7	7	US-11-293-891-4	Sequence 4, App11	636	15	20.8	10	7	US-11-140-487A-1158	Sequence 1158, App
564	15	20.8	7	7	US-11-194-879-17	Sequence 17, App11	637	15	20.8	10	7	US-11-140-487A-1546	Sequence 1546, App
565	15	20.8	7	7	US-11-194-879-38	Sequence 38, App1	638	15	20.8	10	7	US-11-140-487A-1597	Sequence 1597, App
566	15	20.8	7	7	US-11-194-879-44	Sequence 44, App1	639	15	20.8	10	7	US-11-140-487A-1745	Sequence 1745, App
567	15	20.8	8	6	US-10-526-151-28	Sequence 28, App1	640	15	20.8	10	7	US-11-140-487A-1745	Sequence 1911, App
568	15	20.8	8	6	US-10-714-343C-31	Sequence 31, App1	641	15	20.8	10	7	US-11-213-668-5	Sequence 5, App1
569	15	20.8	8	6	US-10-953-613C-646	Sequence 646, App	642	15	20.8	10	7	US-11-122-986-796	Sequence 796, App
570	15	20.8	8	6	US-10-526-060-45	Sequence 45, App1	643	15	20.8	10	7	US-11-263-230-405	Sequence 405, App
571	15	20.8	8	7	US-11-055-093-55	Sequence 55, App1	644	15	20.8	10	7	US-11-263-230-415	Sequence 415, App
572	15	20.8	8	7	US-11-055-093-141	Sequence 141, App	645	15	20.8	10	7	US-11-263-230-425	Sequence 425, App
573	15	20.8	8	7	US-11-055-093-142	Sequence 142, App	646	15	20.8	10	7	US-11-263-230-435	Sequence 435, App
574	15	20.8	8	7	US-11-294-583-2	Sequence 2, App11	647	15	20.8	10	7	US-11-263-230-445	Sequence 445, App
575	15	20.8	8	7	US-11-257-818-57	Sequence 57, App1	648	15	20.8	10	7	US-11-263-230-455	Sequence 455, App
576	15	20.8	8	7	US-11-336-555-6	Sequence 6, App11	649	15	20.8	10	7	US-11-263-230-465	Sequence 465, App
577	15	20.8	8	7	US-11-336-581-15	Sequence 15, App1	650	15	20.8	10	7	US-11-263-230-475	Sequence 475, App
578	15	20.8	9	1	US-09-906-4818-2	Sequence 2, App11	651	15	20.8	10	7	US-11-263-230-485	Sequence 485, App
579	15	20.8	9	6	US-10-497-088-12	Sequence 12, App1	652	15	20.8	10	7	US-11-263-230-503	Sequence 503, App
580	15	20.8	9	6	US-10-508-143A-2	Sequence 2, App11	653	15	20.8	10	7	US-11-263-230-521	Sequence 521, App
581	15	20.8	9	6	US-10-489-071-31	Sequence 31, App1	654	15	20.8	10	7	US-11-263-230-531	Sequence 531, App
582	15	20.8	9	6	US-10-538-066-14	Sequence 14, App1	655	15	20.8	10	7	US-11-339-603-5	Sequence 5, App11
583	15	20.8	9	6	US-10-538-066-66	Sequence 66, App1	656	15	20.8	10	7	US-11-339-603-122	Sequence 122, App
584	15	20.8	9	6	US-10-538-066-140	Sequence 140, App	657	15	20.8	10	7	US-11-293-891-16	Sequence 16, App1
585	15	20.8	9	6	US-10-538-066-141	Sequence 141, App	658	15	20.8	10	7	US-11-257-818-46	Sequence 46, App1
586	15	20.8	9	6	US-10-538-066-676	Sequence 676, App	659	15	20.8	10	7	US-11-099-2838-33	Sequence 33, App1
587	15	20.8	9	6	US-10-985-018-1	Sequence 1, App11	660	15	20.8	10	7	US-11-099-2838-600	Sequence 600, App
588	15	20.8	9	6	US-10-487-890-1	Sequence 1, App11	661	15	20.8	10	7	US-11-242-617-80	Sequence 80, App1
589	15	20.8	9	6	US-10-506-334-5	Sequence 5, App11	662	15	20.8	10	7	US-11-271-805-24	Sequence 24, App1
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591	15	20.8	9	6	US-10-528-563-54	Sequence 54, App1	664	15	20.8	11	6	US-11-330-822-32	Sequence 32, App1
592	15	20.8	9	6	US-10-511-490-1	Sequence 1, App11	665	15	20.8	11	6	US-10-474-853-25	Sequence 25, App1
593	15	20.8	9	6	US-10-511-490-22	Sequence 22, App1	666	15	20.8	11	6	US-10-538-066-214	Sequence 214, App
594	15	20.8	9	7	US-11-055-093-146	Sequence 146, App	667	15	20.8	11	6	US-10-538-066-661	Sequence 661, App
595	15	20.8	9	7	US-11-055-093-147	Sequence 147, App	668	15	20.8	11	6	US-10-506-334-17	Sequence 17, App1
596	15	20.8	9	7	US-11-140-487A-368	Sequence 368, App	669	15	20.8	11	7	US-11-263-537-110	Sequence 110, App1
597	15	20.8	9	7	US-11-140-487A-474	Sequence 474, App	670	15	20.8	11	7	US-11-263-537-110	Sequence 11, App1
598	15	20.8	9	7	US-11-140-487A-634	Sequence 634, App	671	15	20.8	11	7	US-11-263-537-113	Sequence 13, App1
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600	15	20.8	9	7	US-11-140-487A-889	Sequence 889, App	673	15	20.8	11	7	US-11-223-610-166	Sequence 166, App
601	15	20.8	9	7	US-11-140-487A-892	Sequence 892, App	674	15	20.8	12	6	US-10-538-066-678	Sequence 678, App1
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604	15	20.8	9	7	US-11-140-487A-1316	Sequence 1316, App	677	15	20.8	12	6	US-10-531-701-23	Sequence 23, App1
605	15	20.8	9	7	US-11-140-487A-1407	Sequence 1407, App	678	15	20.8	12	6	US-10-502-771-26	Sequence 26, App1
606	15	20.8	9	7	US-11-140-487A-1744	Sequence 1744, App	679	15	20.8	12	6	US-10-953-613C-110	Sequence 110, App
607	15	20.8	9	7	US-11-140-487A-1816	Sequence 1816, App	680	15	20.8	12	6	US-10-953-613C-114	Sequence 114, App
608	15	20.8	9	7	US-11-140-487A-2058	Sequence 2058, App	681	15	20.8	12	6	US-10-953-613C-122	Sequence 122, App
609	15	20.8	9	7	US-11-155-929-52	Sequence 52, App1	682	15	20.8	12	6	US-10-953-613C-129	Sequence 129, App

683	15	20.8	12	6	US-10-953-613C-133	Sequence 133, App
684	15	20.8	12	6	US-10-953-613C-138	Sequence 138, App
685	15	20.8	12	6	US-10-953-613C-159	Sequence 159, App
686	15	20.8	12	6	US-10-953-613C-165	Sequence 165, App
687	15	20.8	12	6	US-10-953-613C-762	Sequence 762, App
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692	15	20.8	13	6	US-10-538-066-679	Sequence 679, App
693	15	20.8	13	6	US-10-538-066-691	Sequence 691, App
694	15	20.8	13	6	US-10-506-334-15	Sequence 15, App1
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696	15	20.8	13	6	US-10-536-804-36	Sequence 36, App1
697	15	20.8	13	6	US-10-953-613C-391	Sequence 391, App
698	15	20.8	13	7	US-11-264-509A-89	Sequence 89, App1
699	15	20.8	13	7	US-11-313-356-13	Sequence 13, App1
700	15	20.8	13	7	US-11-134-871-649	Sequence 649, App
701	15	20.8	13	7	US-11-134-871-893	Sequence 893, App
702	15	20.8	13	7	US-11-373-720-18	Sequence 18, App1
703	15	20.8	14	6	US-10-489-071-3	Sequence 3, App1
704	15	20.8	14	7	US-11-213-668-3	Sequence 119, App
705	15	20.8	14	7	US-11-122-986-119	Sequence 16, App1
706	15	20.8	14	7	US-11-134-871-16	Sequence 1751, App
707	15	20.8	14	7	US-11-134-871-1751	Sequence 147, App
708	15	20.8	14	7	US-11-368-086-147	Sequence 148, App
709	15	20.8	14	7	US-11-368-086-148	Sequence 8, App1
710	15	20.8	15	6	US-10-490-949-5	Sequence 5, App1
711	15	20.8	15	6	US-10-544-499-5	Sequence 967, App
712	15	20.8	15	6	US-10-953-613C-967	Sequence 2209, App
713	15	20.8	15	7	US-11-140-487A-2209	Sequence 629, App
714	15	20.8	15	7	US-11-122-986-629	Sequence 66, App1
715	15	20.8	15	7	US-11-295-192A-66	Sequence 67, App1
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717	15	20.8	15	7	US-11-295-192A-68	Sequence 69, App1
718	15	20.8	15	7	US-11-295-192A-69	Sequence 70, App1
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720	15	20.8	15	7	US-11-295-192A-71	Sequence 72, App1
721	15	20.8	15	7	US-11-295-192A-72	Sequence 73, App1
722	15	20.8	15	7	US-11-295-192A-73	Sequence 74, App1
723	15	20.8	15	7	US-11-295-192A-74	Sequence 75, App1
724	15	20.8	15	7	US-11-295-192A-75	Sequence 76, App1
725	15	20.8	15	7	US-11-295-192A-91	Sequence 91, App1
726	15	20.8	15	7	US-11-295-192A-238	Sequence 238, App
727	15	20.8	15	7	US-11-295-192A-242	Sequence 242, App
728	15	20.8	15	7	US-11-295-192A-243	Sequence 243, App
729	15	20.8	15	7	US-11-295-192A-244	Sequence 244, App
730	15	20.8	15	7	US-11-295-192A-245	Sequence 245, App
731	15	20.8	15	7	US-11-295-192A-318	Sequence 318, App
732	15	20.8	15	7	US-11-295-192A-319	Sequence 319, App
733	15	20.8	15	7	US-11-295-192A-320	Sequence 320, App
734	15	20.8	15	7	US-11-295-192A-321	Sequence 321, App
735	15	20.8	15	7	US-11-295-192A-739	Sequence 739, App
736	15	20.8	15	7	US-11-295-192A-740	Sequence 740, App
737	15	20.8	15	7	US-11-295-192A-907	Sequence 907, App
738	15	20.8	15	7	US-11-295-192A-1175	Sequence 1175, App
739	15	20.8	15	7	US-11-295-192A-1176	Sequence 1177, App
740	15	20.8	15	7	US-11-295-192A-1177	Sequence 1178, App
741	15	20.8	15	7	US-11-295-192A-1178	Sequence 1179, App
742	15	20.8	15	7	US-11-295-192A-1179	Sequence 1180, App
743	15	20.8	15	7	US-11-295-192A-1180	Sequence 1181, App
744	15	20.8	15	7	US-11-295-192A-1181	Sequence 1182, App
745	15	20.8	15	7	US-11-295-192A-1182	Sequence 1183, App
746	15	20.8	15	7	US-11-295-192A-1183	Sequence 1184, App
747	15	20.8	15	7	US-11-295-192A-1184	Sequence 1185, App
748	15	20.8	15	7	US-11-295-192A-1185	Sequence 1186, App
749	15	20.8	15	7	US-11-061-841-405	Sequence 405, App
750	15	20.8	15	7	US-11-350-752-73	Sequence 73, App1
751	15	20.8	15	7	US-11-350-749-73	Sequence 73, App1
752	15	20.8	15	7	US-11-134-871-945	Sequence 945, App
753	15	20.8	15	7	US-11-134-871-1196	Sequence 1196, App
754	15	20.8	15	7	US-11-134-871-2532	Sequence 2532, App
755	15	20.8	15	7	US-11-134-871-3091	Sequence 3091, App

756	15	20.8	15	7	US-11-134-871-3485	Sequence 3485, App
757	15	20.8	15	7	US-11-244-109-8	Sequence 8, App1
758	15	20.8	15	7	US-11-346-079-72	Sequence 72, App1
759	15	20.8	15	7	US-11-346-079-85	Sequence 85, App1
760	15	20.8	15	7	US-11-346-079-89	Sequence 89, App1
761	15	20.8	15	7	US-11-346-079-92	Sequence 92, App1
762	15	20.8	15	7	US-11-361-631-25	Sequence 25, App1
763	14.5	20.1	11	7	US-11-290-249-4	Sequence 4, App1
764	14	19.4	5	6	US-11-338-681-38	Sequence 38, App1
765	14	19.4	5	6	US-10-520-386-3	Sequence 3, App1
766	14	19.4	5	6	US-10-518-941-15	Sequence 15, App1
767	14	19.4	5	7	US-11-139-770A-7	Sequence 7, App1
768	14	19.4	6	6	US-10-525-126-17	Sequence 17, App1
769	14	19.4	6	6	US-10-953-613C-642	Sequence 642, App
770	14	19.4	6	6	US-10-953-613C-750	Sequence 750, App
771	14	19.4	6	7	US-11-257-818-20	Sequence 20, App1
772	14	19.4	6	7	US-11-257-818-29	Sequence 29, App1
773	14	19.4	6	7	US-11-317-846-10	Sequence 10, App1
774	14	19.4	6	7	US-11-327-214-13	Sequence 13, App1
775	14	19.4	7	6	US-10-546-594-94	Sequence 94, App1
776	14	19.4	7	6	US-10-522-086-23	Sequence 23, App1
777	14	19.4	7	7	US-11-271-008-2	Sequence 2, App1
778	14	19.4	7	7	US-11-254-679-81	Sequence 81, App1
779	14	19.4	7	7	US-11-023-959A-26	Sequence 26, App1
780	14	19.4	7	7	US-11-023-959A-56	Sequence 56, App1
781	14	19.4	7	7	US-11-023-959A-59	Sequence 59, App1
782	14	19.4	7	7	US-11-094-133-50	Sequence 50, App1
783	14	19.4	7	7	US-11-263-230-158	Sequence 158, App
784	14	19.4	7	7	US-11-263-230-160	Sequence 160, App
785	14	19.4	7	7	US-11-263-230-143	Sequence 143, App
786	14	19.4	7	7	US-11-263-230-1144	Sequence 1144, App
787	14	19.4	7	7	US-11-263-230-1145	Sequence 1145, App
788	14	19.4	7	7	US-11-263-230-1146	Sequence 1146, App
789	14	19.4	7	7	US-11-263-230-1147	Sequence 1147, App
790	14	19.4	7	7	US-11-263-230-1148	Sequence 1148, App
791	14	19.4	7	7	US-11-263-230-1261	Sequence 1261, App
792	14	19.4	7	7	US-11-261-173-7	Sequence 7, App1
793	14	19.4	7	7	US-11-194-879-5	Sequence 5, App1
794	14	19.4	7	7	US-11-194-879-29	Sequence 29, App1
795	14	19.4	7	7	US-11-194-879-50	Sequence 50, App1
796	14	19.4	8	6	US-10-560-723-185	Sequence 185, App
797	14	19.4	8	6	US-10-449-902-28188	Sequence 28188, App
798	14	19.4	8	7	US-11-122-986-787	Sequence 787, App
799	14	19.4	8	7	US-11-253-223-44	Sequence 44, App1
800	14	19.4	8	7	US-11-194-879-39	Sequence 39, App1

ALIGNMENTS

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RESULT 1
US-10-536-804-74
; Publication 74, Application US/10536804
; Publication No. US20060127908A1
; GENERAL INFORMATION:
; APPLICANT: Williamson, Magali
; TITLE OF INVENTION: Cancer Associated Plexin Bi Mutations
; FILE REFERENCE: 620-373
; CURRENT FILING DATE: 2005-05-27
; PRIOR APPLICATION NUMBER: PCT/GB2003/005223
; PRIOR FILING DATE: 2003-11-28
; PRIOR APPLICATION NUMBER: GB 0227908.1
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 74
; TYPE: PR
; LENGTH: 15
; ORGANISM: Drosophila melanogaster
US-10-536-804-74
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Query Match 40.3%; Score 29; DB 6; Length 15;
Best Local Similarity 53.8%; Pred. No. 49;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 PFSVAKSVKSLYL 14
|||:|||||
Db 3 PFSMKPSVNEIDL 15

RESULT 2

US-10-536-804-76
; Sequence 76, Application US/10536804
; Publication No. US20060127908A1
; GENERAL INFORMATION:
; APPLICANT: Williamson, Magali
; APPLICANT: Masters, John
; TITLE OF INVENTION: Cancer Associated Plexin B1 Mutations
; FILE REFERENCE: 620-373
; CURRENT APPLICATION NUMBER: US/10/536,804
; PRIOR FILING DATE: 2005-05-27
; PRIOR APPLICATION NUMBER: PCT/GB2003/005223
; PRIOR FILING DATE: 2003-11-28
; PRIOR APPLICATION NUMBER: GB 0227908.1
; PRIOR FILING DATE: 2002-11-29
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 76
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-536-804-76

Query Match 36.1%; Score 26; DB 6; Length 15;
Best Local Similarity 53.8%; Pred. No. 1.7e+02;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 PFSVAKSVKSLYL 14
|||:|||||
Db 3 PFSORPSVHALDL 15

RESULT 3

US-11-257-951-1
; Sequence 1, Application US/11257951
; Publication No. US20060140983A1
; GENERAL INFORMATION:
; APPLICANT: Palucka, Anna Karolina
; APPLICANT: Bancheureau, Jacques
; TITLE OF INVENTION: DENDRITIC CELLS LOADED WITH HEAT SHOCKED MELANOMA CELL BODIES
; FILE REFERENCE: BHCS 1013
; CURRENT APPLICATION NUMBER: US/11/257,951
; CURRENT FILING DATE: 2005-10-25
; PRIOR APPLICATION NUMBER: US 60/621,957
; PRIOR FILING DATE: 2004-10-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-11-257-951-1

Query Match 34.7%; Score 25; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSV 5
|||:|||||
Db 5 VPFSV 9

RESULT 4

US-11-254-679-92
; Sequence 92, Application US/11254679
; Publication No. US20060099207A1
; GENERAL INFORMATION:
; APPLICANT: Wu, Herren
; APPLICANT: Allan, Christian
; APPLICANT: Gao, Changshou
; APPLICANT: An, Ling-Ling
; APPLICANT: Klener, Peter
; APPLICANT: Mao, Su-Yau
; APPLICANT: Coyle, Anthony
; TITLE OF INVENTION: High Affinity Antibodies Against HMGBl and Method of Use Thereof
; FILE REFERENCE: HB601US
; CURRENT APPLICATION NUMBER: US/11/254,679
; CURRENT FILING DATE: 2005-10-21
; PRIOR APPLICATION NUMBER: 60/620,726
; PRIOR FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: 60/651,512
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/658,572
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/662,944
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: 60/713,712
; PRIOR FILING DATE: 2005-09-09
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 92
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-254-679-92

Query Match 33.3%; Score 24; DB 7; Length 12;
Best Local Similarity 55.6%; Pred. No. 3.1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 AKSVKSLYL 14
::|||:|||||
Db 3 SOSVSTYL 11

RESULT 5

US-10-538-066-370
; Sequence 370, Application US/10538066
; Publication No. US20060094649A1
; GENERAL INFORMATION:
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, and -B44 Tumor Associated Antigen
; FILE REFERENCE: 2060.01SPC06
; CURRENT APPLICATION NUMBER: US/10/538,066
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US 60/432,017
; PRIOR FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 767
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 370
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-538-066-370

Query Match 31.9%; Score 23; DB 6; Length 11;
Best Local Similarity 66.7%; Pred. No. 4.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 PFSVAK 7
|||:|||||
Db 5 PFSVAK 10

RESULT 6
US-10-522-086-21
; Sequence 21, Application US/10522086
; Publication No. US20060121022A1
; GENERAL INFORMATION:
; APPLICANT: Koga, Takaki
; APPLICANT: Suzuki, Tsukasa
; APPLICANT: Saito, Hiroyuki
; TITLE OF INVENTION: NON-NEUTRALIZING ANTI-aPC ANTIBODIES
; FILE REFERENCE: 14875-138US1
; CURRENT APPLICATION NUMBER: US/10/522,086
; PRIOR FILING DATE: 2005-01-21
; PRIOR APPLICATION NUMBER: PCT/JP2003/009087
; PRIOR FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: JP 2002-212582
; PRIOR FILING DATE: 2002-07-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-522-086-21

Query Match 31.9%; Score 23; DB 6; Length 12;
Best Local Similarity 45.5%; Pred. No. 4.7e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 4 SVAKSVKSLYL 14
: : ||| :
Db 1 TASSSVSSSYL 11

RESULT 7
US-11-298-560-36
; Sequence 36, Application US/11298560
; Publication No. US20060115474A1
; GENERAL INFORMATION:
; APPLICANT: Jacquemin, Marc
; APPLICANT: Saint-Remy, Jean-Marie
; TITLE OF INVENTION: Ligands For Use In Therapeutic Compositions For The Treatment of
; TITLE OF INVENTION: Hemostasis Disorders
; FILE REFERENCE: 50304/110001
; CURRENT APPLICATION NUMBER: US/11/298,560
; CURRENT FILING DATE: 2005-12-09
; PRIOR APPLICATION NUMBER: US 10/030,522
; PRIOR FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: PCT/EP2000/06677
; PRIOR FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: 60/143,891
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: GB9916450.1
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: PCT/BE2004/000118
; PRIOR FILING DATE: 2004-08-16
; PRIOR APPLICATION NUMBER: GB0319118.6
; PRIOR FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: GB0319345.5
; PRIOR FILING DATE: 2003-08-18
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 36
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: KR1X-1 light chain CDRI
US-11-298-560-36

Query Match 31.9%; Score 23; DB 7; Length 12;
Best Local Similarity 55.6%; Pred. No. 4.7e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 6 AKSVKSLYL 14
: : ||| :
Db 3 SQSVASAVL 11

RESULT 8
US-10-538-066-374
; Sequence 374, Application US/10538066
; Publication No. US20060094649A1
; GENERAL INFORMATION:
; APPLICANT: Erimune Inc.
; TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, and -B44 Tumor Associated Antigen
; FILE REFERENCE: 2060.015PC06
; CURRENT APPLICATION NUMBER: US/10/538,066
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US 60/432,017
; PRIOR FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 767
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 374
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-538-066-374

Query Match 30.6%; Score 22; DB 6; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.9e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PPSVA 6
: : ||| :
Db 5 PENVA 9

RESULT 9
US-11-122-986-469
; Sequence 469, Application US/1122986
; Publication No. US20060104989A1
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, ALED
; APPLICANT: DHARAMSI, AKIL
; APPLICANT: VEDADI, MASOUD
; TITLE OF INVENTION: ESSENTIAL NOVEL BACTERIAL POLYPEPTIDES
; FILE REFERENCE: IPT-330.01
; CURRENT APPLICATION NUMBER: US/11/122,986
; CURRENT FILING DATE: 2005-05-05
; PRIOR APPLICATION NUMBER: 60/423,875
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,832
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,915
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,757
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,758
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/424,367
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,376
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,370
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,362
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,373
; PRIOR FILING DATE: 2002-11-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 844
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 469
; LENGTH: 12
; TYPE: PRT

ORGANISM: Enterococcus faecalis
US-11-122-986-469

Query Match
Best Local Similarity 30.6%; Score 22; DB 7; Length 12;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PFSVAK 7
DB 7 PFGVCK 12

RESULT 10

US-11-122-986-506
Sequence 506, Application US/11122986
Publication No. US20060104989A1
GENERAL INFORMATION:

APPLICANT: EDWARDS, ALED
APPLICANT: DHARAMSI, AKIL
APPLICANT: VEDADI, MASOUD
TITLE OF INVENTION: ESSENTIAL NOVEL BACTERIAL POLYPEPTIDES
FILE REFERENCE: IPT-330.01
CURRENT APPLICATION NUMBER: US/11/122,986

PRIOR FILING DATE: 2005-05-05
PRIOR APPLICATION NUMBER: 60/423,875
PRIOR FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: 60/423,832
PRIOR FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: 60/423,915
PRIOR FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: 60/423,757
PRIOR FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: 60/423,758
PRIOR FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: 60/424,367
PRIOR FILING DATE: 2002-11-06
PRIOR APPLICATION NUMBER: 60/424,376
PRIOR FILING DATE: 2002-11-06
PRIOR APPLICATION NUMBER: 60/424,370
PRIOR FILING DATE: 2002-11-06
PRIOR APPLICATION NUMBER: 60/424,362
PRIOR FILING DATE: 2002-11-06
PRIOR APPLICATION NUMBER: 60/424,373
PRIOR FILING DATE: 2002-11-06
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 844
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 506
LENGTH: 12
TYPE: PRT
ORGANISM: Enterococcus faecalis
US-11-122-986-506

Query Match
Best Local Similarity 30.6%; Score 22; DB 7; Length 12;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PFSVAK 7
DB 7 PFGVCK 12

RESULT 11

US-11-330-822-86
Sequence 86, Application US/11330822
Publication No. US20060150281A1
GENERAL INFORMATION:

APPLICANT: GUAN, HANPING
APPLICANT: KEELING, PETER L.
TITLE OF INVENTION: PLANT LIKE STARCHES AND THE METHOD OF MAKING THEM IN
FILE REFERENCE: 15053-04
CURRENT APPLICATION NUMBER: US/11/330,822

CURRENT FILING DATE: 2006-01-11
PRIOR APPLICATION NUMBER: PCT/US98/06660
PRIOR FILING DATE: 1998-04-03
PRIOR APPLICATION NUMBER: 60/042,939
PRIOR FILING DATE: 1997-04-04
NUMBER OF SEQ ID NOS: 86
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 86
LENGTH: 13
TYPE: PRT
ORGANISM: Zea mays
US-11-330-822-86

Query Match
Best Local Similarity 30.6%; Score 22; DB 7; Length 13;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 FSVAKSVKSL 12
DB 4 FSLKKKKKKL 13

RESULT 12
US-11-122-986-737
Sequence 737, Application US/11122986
Publication No. US20060104989A1
GENERAL INFORMATION:

APPLICANT: EDWARDS, ALED
APPLICANT: DHARAMSI, AKIL
APPLICANT: VEDADI, MASOUD
TITLE OF INVENTION: ESSENTIAL NOVEL BACTERIAL POLYPEPTIDES
FILE REFERENCE: IPT-330.01
CURRENT APPLICATION NUMBER: US/11/122,986
PRIOR FILING DATE: 2005-05-05
PRIOR APPLICATION NUMBER: 60/423,875
PRIOR FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: 60/423,832
PRIOR FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: 60/423,915
PRIOR FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: 60/423,757
PRIOR FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: 60/423,758
PRIOR FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: 60/424,367
PRIOR FILING DATE: 2002-11-06
PRIOR APPLICATION NUMBER: 60/424,376
PRIOR FILING DATE: 2002-11-06
PRIOR APPLICATION NUMBER: 60/424,370
PRIOR FILING DATE: 2002-11-06
PRIOR APPLICATION NUMBER: 60/424,362
PRIOR FILING DATE: 2002-11-06
PRIOR APPLICATION NUMBER: 60/424,373
PRIOR FILING DATE: 2002-11-06
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 844
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 737
LENGTH: 15
TYPE: PRT
ORGANISM: Escherichia coli
US-11-122-986-737

Query Match
Best Local Similarity 30.6%; Score 22; DB 7; Length 15;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 SVAKSVKSLYL 14
DB 1 SALLVKKNPYL 11

RESULT 13

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US-11-295-192A-730
; Sequence 730, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Mouter C.
; APPLICANT: Goudsmilt, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 730
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-730
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Query Match          30.6%; Score 22; DB 7; Length 15;
Best Local Similarity 50.0%; Pred. No. 9.3e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
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QY 1 VPFSAKS 8
   :|:|:|:
DB 8 MPVSWAKT 15
```

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RESULT 14
US-11-295-192A-731
; Sequence 731, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Mouter C.
; APPLICANT: Goudsmilt, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 731
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-731
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```
Query Match          30.6%; Score 22; DB 7; Length 15;
Best Local Similarity 50.0%; Pred. No. 9.3e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 VPFSAKS 8
   :|:|:|:
DB 7 MPVSWAKT 14
```

```
RESULT 15
US-11-295-192A-732
; Sequence 732, Application US/11295192A
; Publication No. US20060110803A1
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```
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Mouter C.
; APPLICANT: Goudsmilt, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 732
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-732
```

```
Query Match          30.6%; Score 22; DB 7; Length 15;
Best Local Similarity 50.0%; Pred. No. 9.3e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 VPFSAKS 8
   :|:|:|:
DB 6 MPVSWAKT 13
```

```
RESULT 16
US-11-295-192A-733
; Sequence 733, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Mouter C.
; APPLICANT: Goudsmilt, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 733
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-733
```

```
Query Match          30.6%; Score 22; DB 7; Length 15;
Best Local Similarity 50.0%; Pred. No. 9.3e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 VPFSAKS 8
   :|:|:|:
DB 5 MPVSWAKT 12
```

```
RESULT 17
US-11-295-192A-734
; Sequence 734, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
```

```

; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Goudemilt, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; PRIOR FILING DATE: 2004-06-14
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 734
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-734
```

```

Query Match          30.6%; Score 22; DB 7; Length 15;
Best Local Similarity 50.0%; Pred. No. 9.3e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 VPFSVAKS 8
       :|:|:|:
Db      4 MPVSMAKT 11
```

```

RESULT 18
US-11-295-192A-735
; Sequence 735, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Goudemilt, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; PRIOR FILING DATE: 2004-06-14
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 735
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-735
```

```

Query Match          30.6%; Score 22; DB 7; Length 15;
Best Local Similarity 50.0%; Pred. No. 9.3e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 VPFSVAKS 8
       :|:|:|:
Db      3 MPVSMAKT 10
```

```

RESULT 19
US-11-295-192A-736
; Sequence 736, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Goudemilt, Jaap
```

```

; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; PRIOR FILING DATE: 2004-06-14
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 736
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-736
```

```

Query Match          30.6%; Score 22; DB 7; Length 15;
Best Local Similarity 50.0%; Pred. No. 9.3e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 VPFSVAKS 8
       :|:|:|:
Db      2 MPVSMAKT 9
```

```

RESULT 20
US-11-295-192A-737
; Sequence 737, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Goudemilt, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; PRIOR FILING DATE: 2004-06-14
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 737
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-737
```

```

Query Match          30.6%; Score 22; DB 7; Length 15;
Best Local Similarity 50.0%; Pred. No. 9.3e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 VPFSVAKS 8
       :|:|:|:
Db      1 MPVSMAKT 8
```

```

RESULT 21
US-11-294-583-19
; Sequence 19, Application US/11294583
; Publication No. US20060122122A1
; GENERAL INFORMATION:
; APPLICANT: TOGOSSEI CO., LTD
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES AND USE THEREOF
; FILE REFERENCE: TESHPI02US
; CURRENT APPLICATION NUMBER: US/11/294,583
; PRIOR FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: 2004-352385
; PRIOR FILING DATE: 2004-12-06
; NUMBER OF SEQ ID NOS: 37
```



```

; APPLICANT: Goudsmit, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 239
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-239

Query Match          29.2%; Score 21; DB 7; Length 15;
Best Local Similarity 38.5%; Pred. No. 1.4e+03;
Matches 5; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY      3 FSVAKSVKSLYLIG 15
DB      3 FNTLKPIFKLPLIG 15

RESULT 27
US-11-295-192A-240
; Sequence 240, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Siootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Goudsmit, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 240
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-240

Query Match          29.2%; Score 21; DB 7; Length 15;
Best Local Similarity 38.5%; Pred. No. 1.4e+03;
Matches 5; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY      3 FSVAKSVKSLYLIG 15
DB      2 FNTLKPIFKLPLIG 14

RESULT 28
US-11-295-192A-241
; Sequence 241, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Siootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Goudsmit, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
```

```

; CURRENT APPLICATION NUMBER: US/11/295,192A
; CURRENT FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; PRIOR FILING DATE: 2004-06-14
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 241
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-241

Query Match          29.2%; Score 21; DB 7; Length 15;
Best Local Similarity 38.5%; Pred. No. 1.4e+03;
Matches 5; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY      3 FSVAKSVKSLYLIG 15
DB      1 FNTLKPIFKLPLIG 13

RESULT 29
US-11-295-192A-475
; Sequence 475, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Siootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Goudsmit, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 475
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-475

Query Match          29.2%; Score 21; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VPFS 4
DB      12 VPFS 15

RESULT 30
US-11-295-192A-476
; Sequence 476, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Siootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Goudsmit, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
```

```
; PRIOR FILING DATE: 2004-06-14
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 476
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-476
```

```
Query Match          29.2%; Score 21; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VPFS 4
        ||||
Db       11 VPFS 14
```

```
RESULT 31
US-11-295-192A-477
; Sequence 477, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Goudsmit, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 477
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-477
```

```
Query Match          29.2%; Score 21; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VPFS 4
        ||||
Db       10 VPFS 13
```

```
RESULT 32
US-11-295-192A-478
; Sequence 478, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Goudsmit, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
```

```
; SEQ ID NO 478
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-478
```

```
Query Match          29.2%; Score 21; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VPFS 4
        ||||
Db       9 VPFS 12
```

```
RESULT 33
US-11-295-192A-479
; Sequence 479, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Goudsmit, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 479
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-479
```

```
Query Match          29.2%; Score 21; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VPFS 4
        ||||
Db       8 VPFS 11
```

```
RESULT 34
US-11-295-192A-480
; Sequence 480, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Goudsmit, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 480
; LENGTH: 15
; TYPE: PRT
```

ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide
US-11-295-192A-480

Query Match 29.2%; Score 21; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPPS 4
Db 7 VPPS 10

RESULT 35
US-11-295-192A-481
Sequence 481, Application US/11295192A
Publication No. US20060110803A1
GENERAL INFORMATION:
APPLICANT: Crucell Holland B.V.
APPLICANT: Ter Meulen, Jan H.
APPLICANT: Slootstra, Jelle W.
APPLICANT: Puijk, Mouter C.
TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
FILE REFERENCE: 0089 WO 00 ORD
CURRENT APPLICATION NUMBER: US/11/295,192A
CURRENT FILING DATE: 2005-12-06
PRIOR APPLICATION NUMBER: PCT/EP2004/051102
PRIOR FILING DATE: 2004-06-14
NUMBER OF SEQ ID NOS: 1264
SOFTWARE: PatentIn version 3.1
SEQ ID NO 481
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide
US-11-295-192A-481

Query Match 29.2%; Score 21; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPPS 4
Db 6 VPPS 9

RESULT 36
US-11-295-192A-482
Sequence 482, Application US/11295192A
Publication No. US20060110803A1
GENERAL INFORMATION:
APPLICANT: Crucell Holland B.V.
APPLICANT: Ter Meulen, Jan H.
APPLICANT: Slootstra, Jelle W.
APPLICANT: Puijk, Mouter C.
TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
FILE REFERENCE: 0089 WO 00 ORD
CURRENT APPLICATION NUMBER: US/11/295,192A
CURRENT FILING DATE: 2005-12-06
PRIOR APPLICATION NUMBER: PCT/EP2004/051102
PRIOR FILING DATE: 2004-06-14
NUMBER OF SEQ ID NOS: 1264
SOFTWARE: PatentIn version 3.1
SEQ ID NO 482
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide

US-11-295-192A-482

Query Match 29.2%; Score 21; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPPS 4
Db 5 VPPS 8

RESULT 37
US-11-295-192A-483
Sequence 483, Application US/11295192A
Publication No. US20060110803A1
GENERAL INFORMATION:
APPLICANT: Crucell Holland B.V.
APPLICANT: Ter Meulen, Jan H.
APPLICANT: Slootstra, Jelle W.
APPLICANT: Puijk, Mouter C.
TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
FILE REFERENCE: 0089 WO 00 ORD
CURRENT APPLICATION NUMBER: US/11/295,192A
CURRENT FILING DATE: 2005-12-06
PRIOR APPLICATION NUMBER: PCT/EP2004/051102
PRIOR FILING DATE: 2004-06-14
NUMBER OF SEQ ID NOS: 1264
SOFTWARE: PatentIn version 3.1
SEQ ID NO 483
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide
US-11-295-192A-483

Query Match 29.2%; Score 21; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPPS 4
Db 4 VPPS 7

RESULT 38
US-11-295-192A-484
Sequence 484, Application US/11295192A
Publication No. US20060110803A1
GENERAL INFORMATION:
APPLICANT: Crucell Holland B.V.
APPLICANT: Ter Meulen, Jan H.
APPLICANT: Slootstra, Jelle W.
APPLICANT: Puijk, Mouter C.
TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
FILE REFERENCE: 0089 WO 00 ORD
CURRENT APPLICATION NUMBER: US/11/295,192A
CURRENT FILING DATE: 2005-12-06
PRIOR APPLICATION NUMBER: PCT/EP2004/051102
PRIOR FILING DATE: 2004-06-14
NUMBER OF SEQ ID NOS: 1264
SOFTWARE: PatentIn version 3.1
SEQ ID NO 484
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide
US-11-295-192A-484

Query Match 29.2%; Score 21; DB 7; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFS 4
| | | |
Db 3 VPFS 6

RESULT 39

US-11-295-192A-485
; Sequence 485, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Goudsmit, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 485
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-485

Query Match
Best Local Similarity 29.2%; Score 21; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFS 4
| | | |
Db 2 VPFS 5

RESULT 40

US-11-295-192A-486
; Sequence 486, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Goudsmit, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 486
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-486

Query Match
Best Local Similarity 29.2%; Score 21; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFS 4
| | | |
Db 1 VPFS 4

RESULT 41
US-11-295-192A-729
; Sequence 729, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Goudsmit, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 729
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-729

Query Match
Best Local Similarity 29.2%; Score 21; DB 7; Length 15;
Best Local Similarity 57.1%; Pred. No. 1.4e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VPFSVAK 7
| | | |
Db 9 MPVSMK 15

RESULT 42
US-11-295-192A-738
; Sequence 738, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Goudsmit, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 738
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-738

Query Match
Best Local Similarity 29.2%; Score 21; DB 7; Length 15;
Best Local Similarity 57.1%; Pred. No. 1.4e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PPSVAKS 8
| | | |
Db 1 PVSMAKT 7

```
RESULT 43
US-11-261-429-2
; Sequence 2, Application US/11261429
; Publication No. US20060115899A1
; GENERAL INFORMATION:
; APPLICANT: Buckner, Jane H.
; APPLICANT: Walker, Mindi R.
; TITLE OF INVENTION: METHODS OF GENERATING ANTIGEN-SPECIFIC CD4+CD25+ REGULATORY T
; FILE REFERENCE: BRIVM-1-26413
; CURRENT APPLICATION NUMBER: US/11/261,429
; PRIOR FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: US 60/623,380
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-261-429-2

Query Match          29.2%; Score 21; DB 7; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.4e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      9 VMSLYL 14
|::|||
Db      4 VEALYL 9

RESULT 44
US-11-290-070A-1
; Sequence 1, Application US/11290070A
; Publication No. US20060115478A1
; GENERAL INFORMATION:
; APPLICANT: ZAGHOUBI, Habib
; APPLICANT: GREGG, Randall
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING AND PREVENTING TYPE-1
; FILE REFERENCE: 05062086
; CURRENT APPLICATION NUMBER: US/11/290,070A
; PRIOR FILING DATE: 2005-11-29
; PRIOR APPLICATION NUMBER: US 10/681,788
; PRIOR FILING DATE: 2003-10-08
; PRIOR APPLICATION NUMBER: US 60/371,663
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: PCT/US03/10700
; PRIOR FILING DATE: 2003-04-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Insulin B chain
US-11-290-070A-1.

Query Match          29.2%; Score 21; DB 7; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.4e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      9 VMSLYL 14
|::|||
Db      4 VEALYL 9

RESULT 45
US-11-099-283B-401
; Sequence 401, Application US/11099283B
```

```
; Publication No. US20060134744A1
; GENERAL INFORMATION:
; APPLICANT: HILDEBRAND, WILLIAM H.
; APPLICANT: PRILIMAN, KILEY RAE
; TITLE OF INVENTION: METHOD AND APPARATUS FOR THE PRODUCTION OF ANTIGENS
; FILE REFERENCE: 6680_014
; CURRENT APPLICATION NUMBER: US/11/099,283B
; PRIOR FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/256,410
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/256,409
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 09/465,321
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: 09/974,366
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 401
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; NAME/KEY: MOD_RES
; LOCATION: (3)
; OTHER INFORMATION: Unknown amino acid
US-11-099-283B-401

Query Match          27.8%; Score 20; DB 7; Length 10;
Best Local Similarity 44.4%; Pred. No. 1.4e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      5 VAKSVKSLY 13
|::|||
Db      2 VXPVRSY 10

RESULT 46
US-11-254-679-98
; Sequence 98, Application US/11254679
; Publication No. US20060099207A1
; GENERAL INFORMATION:
; APPLICANT: Wu, Herren
; APPLICANT: Allan, Christian
; APPLICANT: Gao, Changshou
; APPLICANT: An, Ling-Ling
; APPLICANT: Kiener, Peter
; APPLICANT: Mao, Su-Yau
; APPLICANT: Coyle, Anthony
; TITLE OF INVENTION: High Affinity Antibodies Against HMGB1 and Method of Use Thereof
; FILE REFERENCE: HB601US
; CURRENT APPLICATION NUMBER: US/11/254,679
; PRIOR FILING DATE: 2005-10-21
; PRIOR APPLICATION NUMBER: 60/620,726
; PRIOR FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: 60/651,512
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/658,572
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/662,944
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: 60/713,712
; PRIOR FILING DATE: 2005-09-09
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 98
; LENGTH: 12
; TYPE: PRT
```

```

; ORGANISM: Homo sapiens
US-11-254-679-98

Query Match
Best Local Similarity 27.8%; Score 20; DB 7; Length 12;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 6 AKSVKSLYL 14
DB 3 SOSVRSNFL 11

RESULT 47
US-10-564-619-2
; Sequence 2, Application US/10564619
; Publication No. US20060121083A1
; GENERAL INFORMATION:
; APPLICANT: Mor, Amram
; TITLE OF INVENTION: ANTI-MICROBIAL MEDICAL IMPLANTS AND USES THEREOF
; FILE REFERENCE: 31019
; CURRENT APPLICATION NUMBER: US/10/564,619
; CURRENT FILING DATE: 2006-01-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: misc_feature
; OTHER INFORMATION: Possible amidation and aminolauryl added at C'
US-10-564-619-2

Query Match
Best Local Similarity 27.8%; Score 20; DB 6; Length 13;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AKSVKSL 12
DB 1 AKLVKKL 7

RESULT 48
US-11-303-372-83
; Sequence 83, Application US/11303372
; Publication No. US20060100149A1
; GENERAL INFORMATION:
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Lambkin, Imelda J.
; APPLICANT: Pinilla, Clemencia
; APPLICANT: Houghten, Richard
; TITLE OF INVENTION: CONJUGATES OF MEMBRANE TRANSLOCATING AGENTS AND PHARMACEUTICALLY
; FILE REFERENCE: P26,481-A USA
; CURRENT APPLICATION NUMBER: US/11/303,372
; CURRENT FILING DATE: 2005-12-16
; PRIOR APPLICATION NUMBER: US/10/955,656
; PRIOR FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: 10/126,845
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 09/671,089
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/156,246
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 83
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

```

```

; OTHER INFORMATION: D form peptide
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(15)
; OTHER INFORMATION: D form retroinversion peptide
US-11-303-372-83

Query Match
Best Local Similarity 27.8%; Score 20; DB 7; Length 15;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 VPPSVAKSVK 10
DB 6 VPLVVAARK 15

RESULT 49
US-11-303-372-84
; Sequence 84, Application US/11303372
; Publication No. US20060100149A1
; GENERAL INFORMATION:
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Lambkin, Imelda J.
; APPLICANT: Pinilla, Clemencia
; APPLICANT: Houghten, Richard
; TITLE OF INVENTION: CONJUGATES OF MEMBRANE TRANSLOCATING AGENTS AND PHARMACEUTICALLY
; FILE REFERENCE: P26,481-A USA
; CURRENT APPLICATION NUMBER: US/11/303,372
; CURRENT FILING DATE: 2005-12-16
; PRIOR APPLICATION NUMBER: US/10/955,656
; PRIOR FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: 10/126,845
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 09/671,089
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/156,246
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 84
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D form peptide
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(15)
; OTHER INFORMATION: D form retroinversion peptide
US-11-303-372-84

Query Match
Best Local Similarity 27.8%; Score 20; DB 7; Length 15;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 VPPSVAKSVK 10
DB 6 VPLVVAARK 15

RESULT 50
US-11-061-841-310
; Sequence 310, Application US/11061841
; Publication No. US20060122377A1
; GENERAL INFORMATION:
; APPLICANT: DENNIS, MARK S.
; TITLE OF INVENTION: CDR-REPAIRED ANTIBODIES
; FILE REFERENCE: P2070R1
; CURRENT APPLICATION NUMBER: US/11/061,841
; CURRENT FILING DATE: 2005-02-18
; PRIOR APPLICATION NUMBER: US 60/545,840
; PRIOR FILING DATE: 2004-02-19

```

```
/ NUMBER OF SEQ ID NOS: 441
/ SEQ ID NO 310
/ LENGTH: 7
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: Sequence is synthesized.
US-11-061-841-310

Query Match          26.4%; Score 19; DB 7; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.9e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          11 LVLG 15
DB          2 SYLG 6

RESULT 51
US-11-140-487A-79
/ Sequence 79, Application US/11140487A
/ Publication No. US20060093617A1
/ GENERAL INFORMATION:
/ APPLICANT: Immunogenetics N.V.
/ TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C v
/ FILE REFERENCE: 166
/ CURRENT APPLICATION NUMBER: US/11/140,487A
/ PRIOR FILING DATE: 2005-05-31
/ PRIOR APPLICATION NUMBER: EP 04012951.2
/ PRIOR FILING DATE: 2004-06-01
/ PRIOR APPLICATION NUMBER: EP 04447239.7
/ PRIOR FILING DATE: 2004-10-28
/ PRIOR APPLICATION NUMBER: EP 05102441.2
/ PRIOR FILING DATE: 2005-03-25
/ PRIOR APPLICATION NUMBER: US 60/576,310
/ PRIOR FILING DATE: 2004-06-03
/ PRIOR APPLICATION NUMBER: US 60/622,782
/ PRIOR FILING DATE: 2004-10-29
/ PRIOR APPLICATION NUMBER: US 60/665,395
/ PRIOR FILING DATE: 2005-03-25
/ NUMBER OF SEQ ID NOS: 2278
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 79
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: hepatitis C virus
US-11-140-487A-79

Query Match          26.4%; Score 19; DB 7; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY          12 LVLG 15
DB          2 LVLG 5

RESULT 52
US-11-140-487A-175
/ Sequence 175, Application US/11140487A
/ Publication No. US20060093617A1
/ GENERAL INFORMATION:
/ APPLICANT: Immunogenetics N.V.
/ TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C v
/ FILE REFERENCE: 166
/ CURRENT APPLICATION NUMBER: US/11/140,487A
/ PRIOR FILING DATE: 2005-05-31
/ PRIOR APPLICATION NUMBER: EP 04012951.2
/ PRIOR FILING DATE: 2004-06-01
/ PRIOR APPLICATION NUMBER: EP 04447239.7
/ PRIOR FILING DATE: 2004-10-28
/ PRIOR APPLICATION NUMBER: EP 05102441.2
/ PRIOR FILING DATE: 2005-03-25
```

```
/ PRIOR APPLICATION NUMBER: US 60/576,310
/ PRIOR FILING DATE: 2004-06-03
/ PRIOR APPLICATION NUMBER: US 60/622,782
/ PRIOR FILING DATE: 2004-10-29
/ PRIOR APPLICATION NUMBER: US 60/665,395
/ PRIOR FILING DATE: 2005-03-25
/ NUMBER OF SEQ ID NOS: 2278
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 175
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: hepatitis C virus
US-11-140-487A-175

Query Match          26.4%; Score 19; DB 7; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY          12 LVLG 15
DB          2 LVLG 5

RESULT 53
US-11-140-487A-319
/ Sequence 319, Application US/11140487A
/ Publication No. US20060093617A1
/ GENERAL INFORMATION:
/ APPLICANT: Immunogenetics N.V.
/ TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C v
/ FILE REFERENCE: 166
/ CURRENT APPLICATION NUMBER: US/11/140,487A
/ PRIOR FILING DATE: 2005-05-31
/ PRIOR APPLICATION NUMBER: EP 04012951.2
/ PRIOR FILING DATE: 2004-06-01
/ PRIOR APPLICATION NUMBER: EP 04447239.7
/ PRIOR FILING DATE: 2004-10-28
/ PRIOR APPLICATION NUMBER: EP 05102441.2
/ PRIOR FILING DATE: 2005-03-25
/ PRIOR APPLICATION NUMBER: US 60/576,310
/ PRIOR FILING DATE: 2004-06-03
/ PRIOR APPLICATION NUMBER: US 60/622,782
/ PRIOR FILING DATE: 2004-10-29
/ PRIOR APPLICATION NUMBER: US 60/665,395
/ PRIOR FILING DATE: 2005-03-25
/ NUMBER OF SEQ ID NOS: 2278
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 319
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: hepatitis C virus
US-11-140-487A-319

Query Match          26.4%; Score 19; DB 7; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY          12 LVLG 15
DB          2 LVLG 5

RESULT 54
US-11-140-487A-428
/ Sequence 428, Application US/11140487A
/ Publication No. US20060093617A1
/ GENERAL INFORMATION:
/ APPLICANT: Immunogenetics N.V.
/ TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C v
/ FILE REFERENCE: 166
/ CURRENT APPLICATION NUMBER: US/11/140,487A
/ PRIOR FILING DATE: 2005-05-31
/ PRIOR APPLICATION NUMBER: EP 04012951.2
```

```
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: EP 04447239.7
; PRIOR FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: EP 05102441.2
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/576,310
; PRIOR FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: US 60/622,782
; PRIOR FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: US 60/665,395
; PRIOR FILING DATE: 2005-03-25
; NUMBER OF SEQ ID NOS: 2278
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 428
; LENGTH: 9
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-11-140-487A-428
```

```
Query Match          26.4%; Score 19; DB 7; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      12 LYL6 15
       ||:|
Db      3 LYG 6
```

```
RESULT 55
US-11-140-487A-580
; Sequence 580, Application US/11140487A
; Publication No. US20060093617A1
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C vi
; FILE REFERENCE: 166
; CURRENT APPLICATION NUMBER: US/11/140,487A
; PRIOR FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: EP 04012951.2
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: EP 04447239.7
; PRIOR FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: EP 05102441.2
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/576,310
; PRIOR FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: US 60/622,782
; PRIOR FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: US 60/665,395
; PRIOR FILING DATE: 2005-03-25
; NUMBER OF SEQ ID NOS: 2278
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 580
; LENGTH: 9
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-11-140-487A-580
```

```
Query Match          26.4%; Score 19; DB 7; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      12 LYL6 15
       ||:|
Db      4 LYG 7
```

```
RESULT 56
US-11-140-487A-584
; Sequence 584, Application US/11140487A
; Publication No. US20060093617A1
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
```

```
; TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C vi
; FILE REFERENCE: 166
; CURRENT APPLICATION NUMBER: US/11/140,487A
; PRIOR FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: EP 04012951.2
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: EP 04447239.7
; PRIOR FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: EP 05102441.2
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/576,310
; PRIOR FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: US 60/622,782
; PRIOR FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: US 60/665,395
; PRIOR FILING DATE: 2005-03-25
; NUMBER OF SEQ ID NOS: 2278
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 584
; LENGTH: 9
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-11-140-487A-584
```

```
Query Match          26.4%; Score 19; DB 7; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      12 LYL6 15
       ||:|
Db      2 LYG 5
```

```
RESULT 57
US-11-140-487A-638
; Sequence 638, Application US/11140487A
; Publication No. US20060093617A1
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C vi
; FILE REFERENCE: 166
; CURRENT APPLICATION NUMBER: US/11/140,487A
; PRIOR FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: EP 04012951.2
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: EP 04447239.7
; PRIOR FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: EP 05102441.2
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/576,310
; PRIOR FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: US 60/622,782
; PRIOR FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: US 60/665,395
; PRIOR FILING DATE: 2005-03-25
; NUMBER OF SEQ ID NOS: 2278
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 638
; LENGTH: 9
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-11-140-487A-638
```

```
Query Match          26.4%; Score 19; DB 7; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      12 LYL6 15
       ||:|
Db      3 LYG 6
```

```
RESULT 58
```



```
US-11-140-487A-745
; Sequence 745, Application US/11140487A
; Publication No. US20060093617A1
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C vi
; FILE REFERENCE: 166
; CURRENT APPLICATION NUMBER: US/11/140,487A
; PRIOR FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: EP 04012951.2
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: EP 04447239.7
; PRIOR FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: EP 05102441.2
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/576,310
; PRIOR FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: US 60/622,782
; PRIOR FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: US 60/665,395
; PRIOR FILING DATE: 2005-03-25
; NUMBER OF SEQ ID NOS: 2278
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 745
; LENGTH: 9
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-11-140-487A-745
```

```
Query Match      26.4%; Score 19; DB 7; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      12 LVIG 15
        ||:|
        3 LVIG 6
```

```
RESULT 59
US-11-140-487A-1320
; Sequence 1320, Application US/11140487A
; Publication No. US20060093617A1
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C vi
; FILE REFERENCE: 166
; CURRENT APPLICATION NUMBER: US/11/140,487A
; PRIOR FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: EP 04012951.2
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: EP 04447239.7
; PRIOR FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: EP 05102441.2
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/576,310
; PRIOR FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: US 60/622,782
; PRIOR FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: US 60/665,395
; PRIOR FILING DATE: 2005-03-25
; NUMBER OF SEQ ID NOS: 2278
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1320
; LENGTH: 10
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-11-140-487A-1320
```

```
Query Match      26.4%; Score 19; DB 7; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.1e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      7 KSVKSL 12
```

```
Db      1 KEVRSL 6
        ||:|
```

```
RESULT 60
US-11-140-487A-1670
; Sequence 1670, Application US/11140487A
; Publication No. US20060093617A1
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C v
; FILE REFERENCE: 166
; CURRENT APPLICATION NUMBER: US/11/140,487A
; PRIOR FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: EP 04012951.2
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: EP 04447239.7
; PRIOR FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: EP 05102441.2
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/576,310
; PRIOR FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: US 60/622,782
; PRIOR FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: US 60/665,395
; PRIOR FILING DATE: 2005-03-25
; NUMBER OF SEQ ID NOS: 2278
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1670
; LENGTH: 10
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-11-140-487A-1670
```

```
Query Match      26.4%; Score 19; DB 7; Length 10;
Best Local Similarity 75.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
QY      12 LVIG 15
        ||:|
        2 LVIG 5
```

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RESULT 61
US-11-140-487A-1702
; Sequence 1702, Application US/11140487A
; Publication No. US20060093617A1
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C v
; FILE REFERENCE: 166
; CURRENT APPLICATION NUMBER: US/11/140,487A
; PRIOR FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: EP 04012951.2
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: EP 04447239.7
; PRIOR FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: EP 05102441.2
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/576,310
; PRIOR FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: US 60/622,782
; PRIOR FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: US 60/665,395
; PRIOR FILING DATE: 2005-03-25
; NUMBER OF SEQ ID NOS: 2278
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1702
; LENGTH: 10
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-11-140-487A-1702
```

Query Match 26.4%; Score 19; DB 7; Length 10;
Best Local Similarity 75.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 LVIG 15
|:|:|
Db 7 LVIG 10

RESULT 62
US-11-140-487A-1820
; Sequence 1820, Application US/11140487A
; Publication No. US20060093617A1
; GENERAL INFORMATION:
; APPLICANT: Immunogenetics N.V.
; TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C vi
; FILE REFERENCE: 166
; CURRENT APPLICATION NUMBER: US/11/140,487A
; PRIOR FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: EP 04012951.2
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: EP 04447239.7
; PRIOR FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: EP 05102441.2
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/576,310
; PRIOR FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: US 60/622,782
; PRIOR FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: US 60/665,395
; PRIOR FILING DATE: 2005-03-25
; NUMBER OF SEQ ID NOS: 2278
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1820
; LENGTH: 10
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-11-140-487A-1820

Query Match 26.4%; Score 19; DB 7; Length 10;
Best Local Similarity 75.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 LVIG 15
|:|:|
Db 4 LVIG 7

RESULT 63
US-11-134-871-325
; Sequence 325, Application US/11134871
; Publication No. US20060141528A1
; GENERAL INFORMATION:
; APPLICANT: Aebersold, Rudolf H.
; APPLICANT: Zhang, Hui
; TITLE OF INVENTION: Compositions and Methods for
; FILE REFERENCE: 66661-116
; CURRENT APPLICATION NUMBER: US/11/134,871
; CURRENT FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 60/573,593
; PRIOR FILING DATE: 2004-05-21
; NUMBER OF SEQ ID NOS: 3602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 325
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-134-871-325

Query Match 26.4%; Score 19; DB 7; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.1e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VPFSVAK 7
|:|:|
Db 3 VNFVSK 9

RESULT 64
US-10-953-613C-409
; Sequence 409, Application US/10953613C
; Publication No. US20060127404A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Chichi;Heavner, George;Knight, David;Grayeb, John;Scallion;
; APPLICANT: Bernard;Nesspor; Thomas
; TITLE OF INVENTION: HINSE CORE MIMETIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CENS038 NP
; CURRENT APPLICATION NUMBER: US/10/953,613C
; PRIOR FILING DATE: 2004-09-29
; PRIOR APPLICATION NUMBER: 60/507,231
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 1021
; SOFTWARE: PatentIn Ver 3.0
; SEQ ID NO 409
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-953-613C-409

Query Match 26.4%; Score 19; DB 6; Length 11;
Best Local Similarity 50.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PFSVAK 7
|:|:|
Db 6 PYSVQR 11

RESULT 65
US-10-953-613C-119
; Sequence 119, Application US/10953613C
; Publication No. US20060127404A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Chichi;Heavner, George;Knight, David;Grayeb, John;Scallion;
; APPLICANT: Bernard;Nesspor; Thomas
; TITLE OF INVENTION: HINSE CORE MIMETIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CENS038 NP
; CURRENT APPLICATION NUMBER: US/10/953,613C
; CURRENT FILING DATE: 2004-09-29
; PRIOR APPLICATION NUMBER: 60/507,231
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 1021
; SOFTWARE: PatentIn Ver 3.0
; SEQ ID NO 119
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-953-613C-119

Query Match 26.4%; Score 19; DB 6; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PFSVAK 7
|:|:|
Db 7 PYSVQR 12

RESULT 66
US-10-953-613C-123
; Sequence 123, Application US/10953613C
; Publication No. US20060127404A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Chichi;Heavner, George;Knight, David;Grayeb, John;Scallion;
; APPLICANT: Bernard;Nesspor; Thomas

```

; TITLE OF INVENTION: HINGE CORE MIMETIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN5038 NP
; CURRENT APPLICATION NUMBER: US/10/953,613C
; CURRENT FILING DATE: 2004-09-29
; PRIOR APPLICATION NUMBER: 60/507,231
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 1021
; SOFTWARE: PatentIn Ver 3.0
; SEQ ID NO 123
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-953-613C-123

Query Match
26.4%; Score 19; DB 6; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PFSVAK 7
|:|:|:
Db 7 PYSVQR 12

RESULT 67
US-10-953-613C-127
; Sequence 127, Application US/10953613C
; Publication No. US20060127404A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Chichi;Heavner, George;Knight, David;Ghrayeb, John;Scallion,
; APPLICANT: Bernard;Nespor, Thomas
; TITLE OF INVENTION: HINGE CORE MIMETIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN5038 NP
; CURRENT APPLICATION NUMBER: US/10/953,613C
; CURRENT FILING DATE: 2004-09-29
; PRIOR APPLICATION NUMBER: 60/507,231
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 1021
; SOFTWARE: PatentIn Ver 3.0
; SEQ ID NO 127
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-953-613C-127

Query Match
26.4%; Score 19; DB 6; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PFSVAK 7
|:|:|:
Db 7 PYSVQR 12

RESULT 68
US-10-953-613C-131
; Sequence 131, Application US/10953613C
; Publication No. US20060127404A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Chichi;Heavner, George;Knight, David;Ghrayeb, John;Scallion,
; APPLICANT: Bernard;Nespor, Thomas
; TITLE OF INVENTION: HINGE CORE MIMETIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN5038 NP
; CURRENT APPLICATION NUMBER: US/10/953,613C
; CURRENT FILING DATE: 2004-09-29
; PRIOR APPLICATION NUMBER: 60/507,231
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 1021
; SOFTWARE: PatentIn Ver 3.0
; SEQ ID NO 131
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-953-613C-131
```

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Query Match
26.4%; Score 19; DB 6; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PFSVAK 7
|:|:|:
Db 7 PYSVQR 12

RESULT 69
US-10-953-613C-139
; Sequence 139, Application US/10953613C
; Publication No. US20060127404A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Chichi;Heavner, George;Knight, David;Ghrayeb, John;Scallion,
; APPLICANT: Bernard;Nespor, Thomas
; TITLE OF INVENTION: HINGE CORE MIMETIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN5038 NP
; CURRENT APPLICATION NUMBER: US/10/953,613C
; CURRENT FILING DATE: 2004-09-29
; PRIOR APPLICATION NUMBER: 60/507,231
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 1021
; SOFTWARE: PatentIn Ver 3.0
; SEQ ID NO 139
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-953-613C-139

Query Match
26.4%; Score 19; DB 6; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PFSVAK 7
|:|:|:
Db 7 PYSVQR 12

RESULT 70
US-10-953-613C-140
; Sequence 140, Application US/10953613C
; Publication No. US20060127404A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Chichi;Heavner, George;Knight, David;Ghrayeb, John;Scallion,
; APPLICANT: Bernard;Nespor, Thomas
; TITLE OF INVENTION: HINGE CORE MIMETIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN5038 NP
; CURRENT APPLICATION NUMBER: US/10/953,613C
; CURRENT FILING DATE: 2004-09-29
; PRIOR APPLICATION NUMBER: 60/507,231
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 1021
; SOFTWARE: PatentIn Ver 3.0
; SEQ ID NO 140
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-953-613C-140

Query Match
26.4%; Score 19; DB 6; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PFSVAK 7
|:~|:~|:
Db 7 PYSVQR 12

RESULT 71
US-10-953-613C-141
; Sequence 141, Application US/10953613C
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? Publication No. US2006012740A1
? GENERAL INFORMATION:
? APPLICANT: Huang, Chichi;Heavener, George;Knight, David;Ghrayeb, John;Beallon
? APPLICANT: Bernhard;Nesspor, Thomas
? TITLE OF INVENTION: HINGE CORE MINETIBODIES, COMPOSITIONS, METHODS AND USES
? FILE REFERENCE: CEN5038 NP
? CURRENT APPLICATION NUMBER: US/10/953,613C
? CURRENT FILING DATE: 2004-09-29
? PRIOR APPLICATION NUMBER: 60/507,231
? PRIOR FILING DATE: 2003-09-30
? NUMBER OF SEQ ID NOS: 1021
? SOFTWARE: PatentIn Ver 3.0
? SEQ ID NO 141
? LENGTH: 12
? TYPE: PRF
? ORGANISM: Homo sapiens
US-10-953-613C-141

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Query Match	26.4%	Score 19;	DB 6;	Length 12;
Best Local Similarity	50.0%	Pred. No. 2.5e+03;		
Matches	3;	Conservative	2;	Mismatches 1;
				Indels 0;
				Gaps 0

QY	2	PFSVAK	7
		: :	
Db	7	PYSVQR	12

RESULT 72
US-10-953-613C-142
; Sequence 142, Application US/10953613C
; Publication No. US20060127404A1
GENERAL INFORMATION:

APPLICANT: Huang, Chich; Heavner, George; Knight, David; Grayeb, John; Scallon,
APPLICANT: Bernard; Nesspor, Thomas
TITLE OF INVENTION: HINGE CORE MINETRIODIES, COMPOSITIONS, METHODS AND USES
FILE REFERENCE: CEN5038 NP
CURRENT APPLICATION NUMBER: US/10/953,613C
CURRENT FILING DATE: 2004-09-29
PRIOR APPLICATION NUMBER: 60/507,231
PRIOR FILING DATE: 2003-09-30
NUMBER OF SEQ ID NOS: 1021
SOFTWARE: PatentIn Ver 3.0

ORGANISM: Homo sapiens
US-10-953-613C-142

Query Match	26.4%	Score 19;	DB 6;	Length 12;
Best Local Similarity	50.0%	Pred. NO.	2.5e+03;	
Matches	3;	Conservative	2;	Mismatches 1;
				Indels 0;
				Gaps 0;

QY	2	PFSVAK	7
		: :	:
Db	7	PYSVQR	12

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RESULT 73
US-10-953-613C-143
; Sequence 143, Application US/10953613C
; Publication No. US20060127404A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Chichj,Heavner, George,Knight, David,Chrabye, John,Scallont,
; APPLICANT: Bernard,Nesspor,Thomas
; TITLE OF INVENTION: HINCE CORE MIMETIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN5038 NP
; CURRENT APPLICATION NUMBER: US/10/953,613C
; CURRENT FILING DATE: 2004-09-29
; PRIOR APPLICATION NUMBER: 60/507,231
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 1021
; SOFTWARE: PatentIn Ver 3.0
; SEQ ID NO 143

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; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-953-613C-143

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Query Match	26.4%	Score 19;	DB 6;	Length 12;
Best Local Similarity	50.0%;	Pred. No. 2.5e+03;		
Matches	3;	Conservative	2;	Mismatches 1;
				Indels 0;
				Gaps 0;

QY	2	PFSVAK	7
		: :	
Db	7	PYSVQR	12

RESULT 74
US-10-953-613C-144
; Sequence 144, Application US/10953613C
; Publication No. US20060127404A1

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Query Match	26.4%	Score 19;	DB 6;	Length 12;
Best Local Similarity	50.0%;	Pred. No. 2.5e+03;		
Matches	3;	Conservative	2;	Mismatches 1;
				Indels 0;
				Gaps 0;

QY	2	PFSVAK	7
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Db	7	PYSVQR	12

RESULT 75
US-10-953-613C-145
; Sequence 145, Application US/10953613C
; Publication No. US20060127404A1
***** INFORMATION *****

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?
?
? APPLICANT: Huang, Chich;Heaver, George;Knight, David;Grayeb, John;Scallion,
? APPLICANT: Bernard;Nesspor, Thomas
? TITLE OF INVENTION: HINGE CORE MIMETIBODIES, COMPOSITIONS, METHODS AND USES
? FILE REFERENCE: CEN5038 NP
? CURRENT APPLICATION NUMBER: US/10/953,613C
? CURRENT FILING DATE: 2004-09-29
? PRIOR APPLICATION NUMBER: 60/507,231
? PRIOR FILING DATE: 2003-09-30
? NUMBER OF SEQ ID NOS: 1021
? SOFTWARE: PatentIn Ver 3.0
? SEQ ID NO 145
? LENGTH: 12
? TYPE: PRt
? ORGANISM: Homo sapiens
? IS-10-953-613C-145

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Query Match	26.4%	Score 19;	DB 6;	Length 12;
Best Local Similarity	50.0%	Pred. No. 2.5e+03;		
Matches	3;	Conservative	2;	Mismatches 1;
				Indels 0;
				Gaps 0

QY	2	PFSVAK	7
		: :	
Db	7	PYSVQR	12

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RESULT 76
US-10-953-613C-147
; Sequence 147, Application US/10953613C
; Publication No. US20060127404A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Chichi;Heavner, George;Knight, David;Ghrayeb, John;Scallan;
; APPLICANT: Bernard;Nesspor; Thomas
; TITLE OF INVENTION: HINGE CORE MIMETIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN5038 NP
; CURRENT APPLICATION NUMBER: US/10/953,613C
; CURRENT FILING DATE: 2004-09-29
; PRIOR APPLICATION NUMBER: 60/507,231
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 1021
; SOFTWARE: PatentIn Ver 3.0
; SEQ ID NO 147
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-953-613C-147

Query Match      26.4%; Score 19; DB 6; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      2 PFSVAK 7
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Db      7 PYSVOR 12

RESULT 77
US-10-953-613C-148
; Sequence 148, Application US/10953613C
; Publication No. US20060127404A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Chichi;Heavner, George;Knight, David;Ghrayeb, John;Scallan;
; APPLICANT: Bernard;Nesspor; Thomas
; TITLE OF INVENTION: HINGE CORE MIMETIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN5038 NP
; CURRENT APPLICATION NUMBER: US/10/953,613C
; CURRENT FILING DATE: 2004-09-29
; PRIOR APPLICATION NUMBER: 60/507,231
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 1021
; SOFTWARE: PatentIn Ver 3.0
; SEQ ID NO 148
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-953-613C-148

Query Match      26.4%; Score 19; DB 6; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      2 PFSVAK 7
       | : | | :
Db      7 PYSVOR 12

RESULT 78
US-10-953-613C-149
; Sequence 149, Application US/10953613C
; Publication No. US20060127404A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Chichi;Heavner, George;Knight, David;Ghrayeb, John;Scallan;
; APPLICANT: Bernard;Nesspor; Thomas
; TITLE OF INVENTION: HINGE CORE MIMETIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN5038 NP
; CURRENT APPLICATION NUMBER: US/10/953,613C
; CURRENT FILING DATE: 2004-09-29
; PRIOR APPLICATION NUMBER: 60/507,231
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; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 1021
; SOFTWARE: PatentIn Ver 3.0
; SEQ ID NO 149
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-953-613C-149

Query Match      26.4%; Score 19; DB 6; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      2 PFSVAK 7
       | : | | :
Db      7 PYSVOR 12

RESULT 79
US-10-953-613C-150
; Sequence 150, Application US/10953613C
; Publication No. US20060127404A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Chichi;Heavner, George;Knight, David;Ghrayeb, John;Scallan;
; APPLICANT: Bernard;Nesspor; Thomas
; TITLE OF INVENTION: HINGE CORE MIMETIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN5038 NP
; CURRENT APPLICATION NUMBER: US/10/953,613C
; CURRENT FILING DATE: 2004-09-29
; PRIOR APPLICATION NUMBER: 60/507,231
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 1021
; SOFTWARE: PatentIn Ver 3.0
; SEQ ID NO 150
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-953-613C-150

Query Match      26.4%; Score 19; DB 6; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      2 PFSVAK 7
       | : | | :
Db      7 PYSVOR 12

RESULT 80
US-10-953-613C-151
; Sequence 151, Application US/10953613C
; Publication No. US20060127404A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Chichi;Heavner, George;Knight, David;Ghrayeb, John;Scallan;
; APPLICANT: Bernard;Nesspor; Thomas
; TITLE OF INVENTION: HINGE CORE MIMETIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN5038 NP
; CURRENT APPLICATION NUMBER: US/10/953,613C
; CURRENT FILING DATE: 2004-09-29
; PRIOR APPLICATION NUMBER: 60/507,231
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 1021
; SOFTWARE: PatentIn Ver 3.0
; SEQ ID NO 151
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-953-613C-151

Query Match      26.4%; Score 19; DB 6; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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Oy	2	PFSVAK	7
	:	:	:
Db	7	PYSVQR	12

Search completed: July 12, 2006, 05:54:34
Job time : 28 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 12, 2006, 05:30:20 ; Search time 192 Seconds
(without alignments)
35.720 Million cell updates/sec

Title: US-10-671-019-2

Perfect score: 72
Sequence: 1 VPFSVAKSVKSLYLG 15

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 837128

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 800 summaries

Database :

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1: geneseqp1980s:.*
2: geneseqp1980s:.*
3: geneseqp2000s:.*
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5: geneseqp2002s:.*
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7: geneseqp2003bs:.*
8: geneseqp2004s:.*
9: geneseqp2005s:.*
10: geneseqp2006s:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	72	100.0	15	9	ADV91451 Human gro
2	36	50.0	12	2	AAV17975 Peptide S
3	30	41.7	12	9	ADW47130 Ant1-CD20
4	30	41.7	12	9	AEA46220 Apolipop
5	29	40.3	9	9	ADW12121 Human CD2
6	29	40.3	10	8	ADK40054 PNA molec
7	28	38.9	7	8	ADU08556 Heat shoc
8	28	38.9	8	8	ADR65525 Novel hyd
9	28	38.9	8	8	ADU08445 Heat shoc
10	28	38.9	8	8	ADU08841 Heat shoc
11	28	38.9	9	8	ADT73328 Human RSV
12	28	38.9	11	4	AAE00650 Alpha-1,2
13	28	38.9	15	4	AAB97744 gp100 der
14	28	38.9	15	4	AAB97745 gp100 der
15	28	38.9	15	4	AAB98135 Interfero
16	28	38.9	15	4	AAB98135 Interfero
17	28	38.9	15	6	ABP73086 Amino aci
18	28	38.9	15	6	ABR30675 Human can
19	28	38.9	15	6	ABR31599 Human can
20	28	38.9	15	6	ABR31127 Human can
21	28	38.9	15	6	ABR30768 Human can
22	28	38.9	15	6	ABR31373 Human can
23	28	38.9	15	6	ABR30871 Human can

24	28	38.9	15	8	ADN71829	Adn71829 Human 273
25	28	38.9	15	8	ADN71169	Adn71169 Human 273
26	28	38.9	15	8	ADN71392	Adn71392 Human 273
27	28	38.9	15	8	ADN70835	Adn70835 Human 273
28	27.5	38.2	14	3	AAV59641	AAV59641 HIV rep11
29	27.5	38.2	14	5	AAU97491	AAU97491 Human imm
30	27	37.5	11	9	Ad144462	Ad144462 C. dactyl
31	27	37.5	11	9	AEBA28067	AEBA28067 Cynodon d
32	27	37.5	11	9	AEBA13465	AEBA13465 Cynodon d
33	27	37.5	12	2	ADW47132	ADW47132 Ant1-CD20
34	27	37.5	15	4	AAAG64140	AAAG64140 Ribosomal
35	27	37.5	15	7	ADG73517	ADG73517 E faecali
36	27	37.5	15	9	ADV22635	ADV22635 HIV-1 Rev
37	27	37.5	15	9	AEC11117	AEC11117 Enterococ
38	26	36.1	9	8	ADT73298	ADT73298 Human RSV
39	26	36.1	9	8	ADT73299	ADT73299 Human RSV
40	26	36.1	10	8	ADK40048	ADK40048 PNA molec
41	26	36.1	11	6	ABJ36740	ABJ36740 G protein
42	26	36.1	11	8	ADT51155	ADT51155 G protein
43	26	36.1	12	2	AAW25833	AAW25833 T cell ep
44	26	36.1	12	2	AAW25833	AAW25833 HIV B-cel
45	26	36.1	12	2	AAW67349	AAW67349 HIV-1 str
46	26	36.1	12	2	AAW99957	AAW99957 HIV-1 vac
47	26	36.1	12	2	AAU70355	AAU70355 HIV1 chim
48	26	36.1	12	5	AAU70355	AAU70355 Mouse Kap
49	26	36.1	12	8	ADBE25804	ADBE25804 Anti-alph
50	26	36.1	12	8	ADH59661	ADH59661 Light cha
51	26	36.1	12	8	ADH59682	ADH59682 Light cha
52	26	36.1	14	7	ADD90504	ADD90504 Novel hum
53	26	36.1	14	7	ADG90323	ADG90323 Human sec
54	26	36.1	14	9	ADU83344	ADU83344 Nkappa B
55	26	36.1	14	9	ADY25663	ADY25663 Novel hum
56	26	36.1	14	9	AE36996	AE36996 Novel lam
57	26	36.1	14	9	AE36996	AE36996 Novel lam
58	26	36.1	15	2	AAW12084	AAW12084 T-cell ep
59	26	36.1	15	2	AAW11956	AAW11956 T-cell ep
60	26	36.1	15	2	AAW12086	AAW12086 T-cell ep
61	26	36.1	15	2	AAW12085	AAW12085 T-cell ep
62	26	36.1	15	2	AAW12083	AAW12083 T-cell ep
63	26	36.1	15	2	AAW08008	AAW08008 V3 peptid
64	26	36.1	15	5	ABP30990	ABP30990 Peptide #
65	26	36.1	15	5	ABP56426	ABP56426 Human sco
66	26	36.1	15	7	ADAO8653	ADAO8653 Human O77
67	26	36.1	15	7	ADP08996	ADP08996 Secreted
68	26	36.1	15	8	ADN94643	ADN94643 Human 202
69	26	36.1	15	8	ADN94644	ADN94644 Human 202
70	26	36.1	15	8	ADN94062	ADN94062 Human 202
71	26	36.1	15	8	ADN94078	ADN94078 Human ova
72	26	36.1	15	9	ADX17879	ADX17879 Human ova
73	25.5	35.4	14	8	ADM19018	ADM19018 HLA-DR bo
74	25.5	35.4	15	8	ADM19019	ADM19019 HLA-DR bo
75	25	34.7	8	3	AAV77393	AAV77393 HIV-1 gro
76	25	34.7	8	5	ABH76741	ABH76741 Tumour an
77	25	34.7	8	8	ADH62104	ADH62104 Cyclic an
78	25	34.7	8	8	ADP67919	ADP67919 Anti-micr
79	25	34.7	8	8	ADQ28132	ADQ28132 Excluded
80	25	34.7	9	2	AAAR84828	AAAR84828 Modified
81	25	34.7	9	2	AAAR84831	AAAR84831 Modified
82	25	34.7	9	2	AAAR84210	AAAR84210 gp100 mel
83	25	34.7	9	2	AAAR84821	AAAR84821 Modified
84	25	34.7	9	2	AAAR84827	AAAR84827 Modified
85	25	34.7	9	2	AAAR84832	AAAR84832 Modified
86	25	34.7	9	2	AAAR84833	AAAR84833 Modified
87	25	34.7	9	2	AAAR84829	AAAR84829 Modified
88	25	34.7	9	2	AAAR84822	AAAR84822 Modified
89	25	34.7	9	2	AAAR84830	AAAR84830 Modified
90	25	34.7	9	2	AAAR84834	AAAR84834 Modified
91	25	34.7	9	2	AAAR84820	AAAR84820 Modified
92	25	34.7	9	2	AAAR84823	AAAR84823 Modified
93	25	34.7	9	2	AAAR84816	AAAR84816 Modified
94	25	34.7	9	2	AAAR84817	AAAR84817 Modified
95	25	34.7	9	2	AAAR84824	AAAR84824 Modified
96	25	34.7	9	2	AAAR84825	AAAR84825 Modified

97	25	34.7	9	2	AAE84826	AAE84826 Modified	170	25	34.7	9	5	ABG79042	ABG79042 Human Gp1
98	25	34.7	9	2	AAE84835	AAE84835 Modified	171	25	34.7	9	5	AAO17085	AAO17085 Gp 100 an
99	25	34.7	9	2	AAE84818	AAE84818 Modified	172	25	34.7	9	5	AAO18865	AAO18865 Human gp1
100	25	34.7	9	2	AAE84819	AAE84819 Modified	173	25	34.7	9	5	AAE26788	AAE26788 Human gp1
101	25	34.7	9	2	AAE84836	AAE84836 Modified	174	25	34.7	9	5	AAU09706	AAU09706 Human gp1
102	25	34.7	9	2	AAW70018	AAW70018 Melanoma-	175	25	34.7	9	5	AAU09696	AAU09696 Anti-mela
103	25	34.7	9	2	AAW71117	AAW71117 Human bcl1	176	25	34.7	9	5	ABG66780	ABG66780 Tumour an
104	25	34.7	9	2	AAW54599	AAW54599 Peptide 4	177	25	34.7	9	5	ABG80131	ABG80131 MHC class
105	25	34.7	9	2	AAW78851	AAW78851 PMEL 17 (178	25	34.7	9	5	AAE17297	AAE17297 gp100-mod
106	25	34.7	9	2	AAW77120	AAW77120 gp100/Pme	179	25	34.7	9	5	AEA36294	AEA36294 Human gp1
107	25	34.7	9	2	AAV10448	AAV10448 HLA Class	180	25	34.7	9	6	AAE36055	AAE36055 Tumour as
108	25	34.7	9	2	AAV40214	AAV40214 Amino ac1	181	25	34.7	9	6	AAE79857	AAE79857 Human can
109	25	34.7	9	2	AAV47617	AAV47617 Immunogen	182	25	34.7	9	6	AAE35575	AAE35575 Melanoma
110	25	34.7	9	2	AAV33113	AAV33113 Human gp1	183	25	34.7	9	6	ABR56418	ABR56418 Human mel
111	25	34.7	9	2	AAV53527	AAV53527 Human mel	184	25	34.7	9	6	ABJ19877	ABJ19877 MHC bind1
112	25	34.7	9	2	AAV26870	AAV26870 Melanoma-	185	25	34.7	9	6	ABR08668	ABR08668 Cancer ce
113	25	34.7	9	2	AAV00716	AAV00716 Tumour an	186	25	34.7	9	6	ABR05539	ABR05539 Human can
114	25	34.7	9	2	AAV49654	AAV49654 Tumour an	187	25	34.7	9	6	ABR05668	ABR05668 Human can
115	25	34.7	9	2	AAV01754	AAV01754 Exemplary	188	25	34.7	9	6	ABR44519	ABR44519 Human mel
116	25	34.7	9	3	AAV1521	AAV1521 Human gp1	189	25	34.7	9	6	ABU96615	ABU96615 MHC class
117	25	34.7	9	3	AAV90804	AAV90804 Human leu	190	25	34.7	9	6	ADA19547	ADA19547 Human can
118	25	34.7	9	3	AAV84766	AAV84766 Antigenic	191	25	34.7	9	6	ADA89157	ADA89157 Gp100-der
119	25	34.7	9	3	AAV84770	AAV84770 Antigenic	192	25	34.7	9	7	AAE38651	AAE38651 HLA-A2 re
120	25	34.7	9	3	AAE33663	AAE33663 MHC class	193	25	34.7	9	7	ADB97734	ADB97734 Human gp1
121	25	34.7	9	3	AAE23680	AAE23680 Cytotoxic	194	25	34.7	9	7	ADB97733	ADB97733 Human gp1
122	25	34.7	9	3	AAV92300	AAV92300 gp100-Pme	195	25	34.7	9	7	ADB97751	ADB97751 Human gp1
123	25	34.7	9	3	AAV56615	AAV56615 gp100-Pme	196	25	34.7	9	7	ADB97742	ADB97742 Human gp1
124	25	34.7	9	3	AAV84297	AAV84297 Tumour as	197	25	34.7	9	7	ADB97735	ADB97735 Human gp1
125	25	34.7	9	3	AAV82980	AAV82980 gp100(Pme	198	25	34.7	9	7	ADB97744	ADB97744 Human gp1
126	25	34.7	9	3	AAE02623	AAE02623 Tumour as	199	25	34.7	9	7	ADB97740	ADB97740 Human gp1
127	25	34.7	9	3	AAE08695	AAE08695 Antigenic	200	25	34.7	9	7	ADB97750	ADB97750 Human gp1
128	25	34.7	9	3	AAE02112	AAE02112 gp100 Pme	201	25	34.7	9	7	ADB97732	ADB97732 Human gp1
129	25	34.7	9	4	AAE95909	AAE95909 MHC class	202	25	34.7	9	7	ADB97737	ADB97737 Human gp1
130	25	34.7	9	4	AAE93759	AAE93759 Human Pme	203	25	34.7	9	7	ADB97739	ADB97739 Human gp1
131	25	34.7	9	4	AAE02662	AAE02662 Human mel	204	25	34.7	9	7	ADB97752	ADB97752 Human gp1
132	25	34.7	9	4	AAU28973	AAU28973 Modified	205	25	34.7	9	7	ADB97749	ADB97749 Human gp1
133	25	34.7	9	4	AAU28974	AAU28974 Modified	206	25	34.7	9	7	ADB97697	ADB97697 Human mel
134	25	34.7	9	4	AAU28965	AAU28965 Modified	207	25	34.7	9	7	ADB97738	ADB97738 Human gp1
135	25	34.7	9	4	AAU28976	AAU28976 Modified	208	25	34.7	9	7	ADB97743	ADB97743 Human gp1
136	25	34.7	9	4	AAU28970	AAU28970 Modified	209	25	34.7	9	7	ADB97747	ADB97747 Human gp1
137	25	34.7	9	4	AAU28972	AAU28972 Modified	210	25	34.7	9	7	ADB97748	ADB97748 Human gp1
138	25	34.7	9	4	AAU28977	AAU28977 Modified	211	25	34.7	9	7	ADB97736	ADB97736 Human gp1
139	25	34.7	9	4	AAU28983	AAU28983 Modified	212	25	34.7	9	7	ADB97745	ADB97745 Human gp1
140	25	34.7	9	4	AAU28968	AAU28968 Modified	213	25	34.7	9	7	ADB97746	ADB97746 Human gp1
141	25	34.7	9	4	AAU28978	AAU28978 Modified	214	25	34.7	9	7	ADB97741	ADB97741 Human gp1
142	25	34.7	9	4	AAU28981	AAU28981 Modified	215	25	34.7	9	7	ADW31065	ADW31065 HLA bind1
143	25	34.7	9	4	AAU28984	AAU28984 Modified	216	25	34.7	9	7	ADW31097	ADW31097 HLA bind1
144	25	34.7	9	4	AAU28979	AAU28979 Modified	217	25	34.7	9	7	ADW31056	ADW31056 HLA bind1
145	25	34.7	9	4	AAU28985	AAU28985 Modified	218	25	34.7	9	7	ADW31062	ADW31062 HLA bind1
146	25	34.7	9	4	AAU28971	AAU28971 Modified	219	25	34.7	9	7	ADW31063	ADW31063 HLA bind1
147	25	34.7	9	4	AAU28980	AAU28980 Modified	220	25	34.7	9	7	ADW31069	ADW31069 HLA bind1
148	25	34.7	9	4	AAU28930	AAU28930 gp100 imm	221	25	34.7	9	7	ADW31054	ADW31054 HLA bind1
149	25	34.7	9	4	AAU28967	AAU28967 Modified	222	25	34.7	9	7	ADW31077	ADW31077 HLA bind1
150	25	34.7	9	4	AAU28975	AAU28975 Modified	223	25	34.7	9	7	ADW31060	ADW31060 HLA bind1
151	25	34.7	9	4	AAU28966	AAU28966 Modified	224	25	34.7	9	7	ADW31058	ADW31058 HLA bind1
152	25	34.7	9	4	AAU28969	AAU28969 Modified	225	25	34.7	9	7	ADW31064	ADW31064 HLA bind1
153	25	34.7	9	4	AAU28982	AAU28982 Modified	226	25	34.7	9	7	ADW31067	ADW31067 HLA bind1
154	25	34.7	9	4	AAU28932	AAU28932 Anti-mela	227	25	34.7	9	7	ADW31082	ADW31082 HLA bind1
155	25	34.7	9	4	AAU28958	AAU28958 Anti-mela	228	25	34.7	9	7	ADW31059	ADW31059 HLA bind1
156	25	34.7	9	4	AAU28954	AAU28954 Anti-mela	229	25	34.7	9	7	ADW31061	ADW31061 HLA bind1
157	25	34.7	9	4	AAU28953	AAU28953 Anti-mela	230	25	34.7	9	7	ADW31051	ADW31051 HLA bind1
158	25	34.7	9	4	AAU28959	AAU28959 Anti-mela	231	25	34.7	9	7	ADW31068	ADW31068 HLA bind1
159	25	34.7	9	4	AAU28955	AAU28955 Anti-mela	232	25	34.7	9	7	ADW31562	ADW31562 HLA bind1
160	25	34.7	9	4	AAU28956	AAU28956 Anti-mela	233	25	34.7	9	7	ADW31057	ADW31057 HLA bind1
161	25	34.7	9	4	AAU28957	AAU28957 Anti-mela	234	25	34.7	9	7	ADW31066	ADW31066 HLA bind1
162	25	34.7	9	4	AAU28952	AAU28952 Human mel	235	25	34.7	9	8	ADG89608	ADG89608 Class I H
163	25	34.7	9	4	AAU28951	AAU28951 gp100 mel	236	25	34.7	9	8	ADG20340	ADG20340 Antigenic
164	25	34.7	9	4	AAU28950	AAU28950 gp100 mel	237	25	34.7	9	8	ADJ36372	ADJ36372 Human mel
165	25	34.7	9	4	AAU28949	AAU28949 Cancer ce	238	25	34.7	9	8	ADK69070	ADK69070 Epitope 1
166	25	34.7	9	4	AAU28948	AAU28948 Tumour-as	239	25	34.7	9	8	ADM12462	ADM12462 MHC class
167	25	34.7	9	4	AAU28947	AAU28947 Exemplary	240	25	34.7	9	8	ADM17856	ADM17856 Tumour as
168	25	34.7	9	4	AAU28946	AAU28946 Human gp1	241	25	34.7	9	8	ADM17852	ADM17852 Human tum
169	25	34.7	9	4	AAU28945	AAU28945 Human gp1	242	25	34.7	9	8	ADM17851	ADM17851 Human gp1

243	25	34.7	9	8	AD043392	Ad043392 Human tum	316	25	34.7	15	6	ABR37165	Ab37165 Human can
244	25	34.7	9	8	AD010868	Ad010868 Homo sapi	317	25	34.7	15	6	ABR36781	Ab36781 Human can
245	25	34.7	9	8	AD087048	Ad087048 Human gen	318	25	34.7	15	6	ABR37398	Ab37398 Human can
246	25	34.7	9	8	AD0869741	Ad0869741 Novel hyd	319	25	34.7	15	6	ABR00910	Ab00910 Bioactive
247	25	34.7	9	8	AD0552359	Ad0552359 HLA-A2 re	320	25	34.7	15	8	ADN71198	Adn71198 Human 273
248	25	34.7	9	8	AD0575029	Ad0575029 Human mel	321	25	34.7	15	8	ADN71619	Adn71619 Human 273
249	25	34.7	9	8	AD0581348	Ad0581348 Tumour-as	322	25	34.7	15	9	ADV22141	Adv22141 SHIV env
250	25	34.7	9	8	ADT73579	Adt73579 Human RSV	323	25	34.7	15	9	ADM78280	Adm78280 Mouse neu
251	25	34.7	9	8	ADT73578	Adt73578 Human RSV	324	25	34.7	15	9	ADM78288	Adm78288 Rat DEF d
252	25	34.7	9	8	ADT25862	Adt25862 Human mel	325	25	34.7	15	10	AE066548	Ae066548 Peptide f
253	25	34.7	9	8	ADU08482	Adu08482 Cancer an	326	25	34.7	7	5	ABP67285	Abp67285 Human CD6
254	25	34.7	9	8	ADU08497	Adu08497 IMD ,pepti	327	25	34.7	8	2	AA1Y16811	Aay16811 Heat choc
255	25	34.7	9	8	ADU87382	Adu87382 Human mel	328	25	34.7	8	5	ABP67278	Abp67278 Human CD6
256	25	34.7	9	9	ADU69291	Adu69291 HIV-1 gp1	329	25	34.7	8	7	ADP67279	Adp67279 Human CD6
257	25	34.7	9	9	ADM13784	Adm13784 Human mel	330	25	34.7	8	7	ADP67281	Adp67281 Heat choc
258	25	34.7	9	9	ADM12146	Adm12146 Human CD2	331	25	34.7	8	8	ADK09058	Adk09058 Human pap
259	25	34.7	9	9	ADK08558	Adk08558 Class I H	332	25	34.7	8	8	ADU08595	Adu08595 Heat choc
260	25	34.7	9	9	ADY26211	Ady26211 MHC Class	333	25	34.7	8	9	ADV34214	Adv34214 Consensus
261	25	34.7	9	9	ADZ020248	Adz020248 Cander im	334	25	34.7	9	3	AA0808572	Aa0808572 Peptide i
262	25	34.7	9	9	ADZ67829	Adz67829 Majdr his	335	25	34.7	9	5	AA028752	Aa028752 Human CAS
263	25	34.7	9	9	AE028684	Ae028684 Human leu	336	25	34.7	9	5	ABP67273	Abp67273 Human CD6
264	25	34.7	9	9	AEC92213	Aec92213 Melanoma	337	25	34.7	9	5	ABP67274	Abp67274 Human CD6
265	25	34.7	9	9	AEC92214	Aec92214 Melanoma	338	25	34.7	9	6	ABP75230	Abp75230 Chlamydia
266	25	34.7	9	9	AED14746	Aed14746 Peptide f	339	25	34.7	9	6	ABR04765	Ab04765 Human can
267	25	34.7	9	10	AE01627	Ae01627 HLA-A0201	340	25	34.7	9	6	ABR05751	Ab05751 Human can
268	25	34.7	9	10	AE01170	Ae01170 Melanocyte	341	25	34.7	9	6	ABR05919	Ab05919 Human can
269	25	34.7	10	2	AAW29931	Aaw29931 Rat isp. A	342	25	34.7	9	6	ABR24011	Ab24011 Human can
270	25	34.7	10	2	AAW29915	Aaw29915 Porcine A	343	25	34.7	9	6	ABR23820	Ab23820 Human can
271	25	34.7	10	2	AA1Y10450	Aay10450 HLA Class	344	25	34.7	9	6	ABR05106	Ab05106 Human can
272	25	34.7	10	4	AAU28931	Aau28931 gp100 imm	345	25	34.7	9	6	ABR04896	Ab04896 Human can
273	25	34.7	10	4	AAU71990	Aau71990 gp100 mel	346	25	34.7	9	6	ABR05876	Ab05876 Human can
274	25	34.7	10	4	AA094017	Aa094017 Human com	347	25	34.7	9	6	ABR05670	Ab05670 Human can
275	25	34.7	10	4	AA086348	Aa086348 Saccharom	348	25	34.7	9	8	ADN68721	Adn68721 Human 273
276	25	34.7	10	5	AB080133	Ab080133 MHC class	349	25	34.7	9	8	ADN67589	Adn67589 Human 273
277	25	34.7	10	6	ABR05642	Ab05642 Human can	350	25	34.7	9	8	ADN67344	Adn67344 Human 273
278	25	34.7	10	6	ABR06013	Ab06013 Human can	351	25	34.7	9	8	ADN69490	Adn69490 Human 273
279	25	34.7	10	6	ABR91263	Ab91263 P. papata	352	25	34.7	10	3	AA1Y81466	Aay81466 E. coli "
280	25	34.7	10	7	AD097698	Ad097698 Human mel	353	25	34.7	10	4	AA095531	Aa095531 Human com
281	25	34.7	10	8	ADK40049	Adk40049 PNA 'molec	354	25	34.7	10	4	AAW42903	Aaw42903 Mycoplasma
282	25	34.7	10	8	ADK69072	Adk69072 Eptlope 1	355	25	34.7	10	4	AAW43172	Aaw43172 Mycoplasma
283	25	34.7	10	8	ADN91507	Adn91507 Human 202	356	25	34.7	10	5	AB051836	Ab051836 Human 34P
284	25	34.7	10	8	ADN93796	Adn93796 Human 202	357	25	34.7	10	5	AB051606	Ab051606 Human 34P
285	25	34.7	10	8	ADN93977	Adn93977 Human 202	358	25	34.7	10	5	AB051536	Ab051536 Human 34P
286	25	34.7	10	8	ADN93487	Adn93487 Human 202	359	25	34.7	10	5	AB051906	Ab051906 Human 34P
287	25	34.7	10	8	ADN90273	Adn90273 Human 202	360	25	34.7	10	5	ABP67269	Abp67269 Human CD6
288	25	34.7	10	8	ADN91212	Adn91212 Human 202	361	25	34.7	10	5	ABP67270	Abp67270 Human CD6
289	25	34.7	10	8	ADN91830	Adn91830 Human 202	362	25	34.7	10	6	ABR06022	Ab06022 Human can
290	25	34.7	10	8	ADN93858	Adn93858 Human 202	363	25	34.7	10	6	ABR05003	Ab05003 Human can
291	25	34.7	10	8	ADQ10870	Adq10870 Homo sapi	364	25	34.7	10	6	ABR24316	Ab24316 Human can
292	25	34.7	10	8	ADS01350	Ad01350 Tumour-as	365	25	34.7	10	6	ABR23958	Ab23958 Human can
293	25	34.7	11	2	AAW23266	Aaw23266 Tumour ne	366	25	34.7	10	6	ABR24126	Ab24126 Human can
294	25	34.7	11	6	ABR91265	Ab91265 P. papata	367	25	34.7	10	6	ABR05252	Ab05252 Human can
295	25	34.7	12	5	ABP67265	Abp67265 Human CD6	368	25	34.7	10	6	ABR05620	Ab05620 Human can
296	25	34.7	12	8	AD042769	Ad042769 Leader se	369	25	34.7	10	6	ABR05843	Ab05843 Human can
297	25	34.7	13	4	AA088001	Aa088001 CD66 pept	370	25	34.7	10	6	ABR06035	Ab06035 Human can
298	25	34.7	13	5	ABP67241	Abp67241 Human CD6	371	25	34.7	10	6	ABR05783	Ab05783 Human can
299	25	34.7	13	8	ADG78907	Adg78907 Control p	372	25	34.7	10	6	ABR05662	Ab05662 Human can
300	25	34.7	13	8	ADN48981	Adn48981 Control p	373	25	34.7	10	6	ABR05853	Ab05853 Human can
301	25	34.7	13	9	AED0661	Aed0661 PNC-29 co	374	25	34.7	10	8	ADN67806	Adn67806 Human 273
302	25	34.7	14	2	AA05280	Aa05280 Human int	375	25	34.7	10	8	ADN70212	Adn70212 Human 273
303	25	34.7	15	1	AA090266	Aa090266 Antigenic	376	25	34.7	10	8	ADN67782	Adn67782 Human 273
304	25	34.7	15	2	AA094865	Aa094865 Peptide f	377	25	34.7	10	8	ADP25590	Adp25590 Plasmodiu
305	25	34.7	15	2	AAW43543	Aaw43543 Mycobacte	378	25	34.7	10	8	ADP10571	Adp10571 Penicilli
306	25	34.7	15	2	AA1Y1511	Aay1511 Human neu	379	25	34.7	11	5	ABP67268	Abp67268 Human CD6
307	25	34.7	15	2	ABP24463	Abp24463 HIV DR su	380	25	34.7	11	5	ABP67267	Abp67267 Human CD6
308	25	34.7	15	4	AA015130	Aa015130 Human pot	381	25	34.7	11	5	ABP67266	Abp67266 Human CD6
309	25	34.7	15	6	ABR31541	Ab31541 Human can	382	25	34.7	12	2	ABR00885	Ab00885 Bioactive
310	25	34.7	15	6	ABR30594	Ab30594 Human can	383	25	34.7	12	2	AA042324	Aa042324 EBV VCA p
311	25	34.7	15	6	ABR36884	Ab36884 Human can	384	25	34.7	12	2	ABR42323	Ab42323 EBV VCA p
312	25	34.7	15	6	ABR37666	Ab37666 Human can	385	25	34.7	12	5	ABP67264	Abp67264 Human CD6
313	25	34.7	15	6	ABR37751	Ab37751 Human can	386	25	34.7	12	9	ADW47131	Adw47131 Act1-CD20
314	25	34.7	15	6	ABR37259	Ab37259 Human can	387	25	34.7	12	9	ADX18723	Adx18723 Novel kin
315	25	34.7	15	6	ABR30841	Ab30841 Human can	388	25	34.7	12	9	ADX18773	Adx18773 Novel kin

389	24	33.3	12	9	AEA53687	Aea53687	Novel hum	462	23	31.9	11	2	AAW23253	AAw23253	Tumour ne
390	24	33.3	12	9	AEA53697	Aea53697	Novel hum	463	23	31.9	11	2	AAW95055	AaW95055	peptide f
391	24	33.3	12	9	AEC00606	Aec00606	Phosphata	464	23	31.9	11	2	ABR62533	AbR62533	Human hrti
392	24	33.3	12	9	AEC00556	Aec00556	Serine/Th	465	23	31.9	11	8	ADN64530	AdN64530	H1A bindi
393	24	33.3	13	2	AAW70636	AaW70636	Sequence	466	23	31.9	11	8	ADP66671	AdP66671	Rat heat
394	24	33.3	13	2	AAW70636	AaW70636	Second ge	467	23	31.9	11	8	ADP66671	AdP66671	Rat heat
395	24	33.3	13	4	ABR88002	AbR88002	CD66 pep	468	23	31.9	11	10	AEF11076	AeF11076	Human H1A
396	24	33.3	13	4	ABR88002	AbR88002	CD66 pep	469	23	31.9	11	10	AEF11076	AeF11076	Human H1A
397	24	33.3	13	7	ABJ38801	AbJ38801	Human G-P	470	23	31.9	12	2	AAW29713	AaW29713	TNF recep
398	24	33.3	13	6	ADM35590	AdM35590	HLA bindi	471	23	31.9	12	2	AAW29713	AaW29713	TNF recep
399	24	33.3	13	7	ADM35590	AdM35590	HLA bindi	472	23	31.9	12	2	AAW29713	AaW29713	TNF recep
400	24	33.3	13	8	ADM35590	AdM35590	HLA bindi	473	23	31.9	12	3	AAW29713	AaW29713	TNF recep
401	24	33.3	13	8	ADM35590	AdM35590	HLA bindi	474	23	31.9	12	3	AAW29713	AaW29713	TNF recep
402	24	33.3	13	8	ADM35590	AdM35590	HLA bindi	475	23	31.9	12	3	AAW29713	AaW29713	TNF recep
403	24	33.3	13	10	AEF95628	AeF95628	Human epi	476	23	31.9	12	5	ABR75949	AbR75949	Human KRP
404	24	33.3	13	10	AEF95628	AeF95628	Human epi	477	23	31.9	12	5	ABR75949	AbR75949	Human KRP
405	24	33.3	14	4	AAW97374	AaW97374	Human pep	478	23	31.9	12	5	AAW97374	AaW97374	Human KRP
406	24	33.3	14	4	AAW97374	AaW97374	Human pep	479	23	31.9	12	5	AAW97374	AaW97374	Human KRP
407	24	33.3	14	4	AAW97374	AaW97374	Human pep	480	23	31.9	12	5	AAW97374	AaW97374	Human KRP
408	24	33.3	14	4	AAW97374	AaW97374	Human pep	481	23	31.9	12	5	AAW97374	AaW97374	Human KRP
409	24	33.3	15	4	AAW98637	AaW98637	Alpha1-an	482	23	31.9	12	5	AAW98637	AaW98637	Alpha1-an
410	24	33.3	15	5	AAW98637	AaW98637	Alpha1-an	483	23	31.9	12	5	AAW98637	AaW98637	Alpha1-an
411	24	33.3	15	5	AAW98637	AaW98637	Alpha1-an	484	23	31.9	12	5	AAW98637	AaW98637	Alpha1-an
412	24	33.3	15	6	ABR31082	AbR31082	Human can	485	23	31.9	12	6	ADN90308	AdN90308	MS-Roc
413	24	33.3	15	6	ABR31082	AbR31082	Human can	486	23	31.9	12	6	ADN90308	AdN90308	MS-Roc
414	24	33.3	15	6	ABR31082	AbR31082	Human can	487	23	31.9	12	6	ADN90308	AdN90308	MS-Roc
415	24	33.3	15	6	ABR31082	AbR31082	Human can	488	23	31.9	12	6	ADN90308	AdN90308	MS-Roc
416	24	33.3	15	6	ABR31082	AbR31082	Human can	489	23	31.9	12	6	ADN90308	AdN90308	MS-Roc
417	24	33.3	15	6	ABR31082	AbR31082	Human can	490	23	31.9	12	6	ADN90308	AdN90308	MS-Roc
418	24	33.3	15	6	ABR31082	AbR31082	Human can	491	23	31.9	12	6	ADN90308	AdN90308	MS-Roc
419	24	33.3	15	6	ABR31082	AbR31082	Human can	492	23	31.9	12	6	ADN90308	AdN90308	MS-Roc
420	24	33.3	15	6	ABR31082	AbR31082	Human can	493	23	31.9	12	6	ADN90308	AdN90308	MS-Roc
421	24	33.3	15	6	ABR31082	AbR31082	Human can	494	23	31.9	12	6	ADN90308	AdN90308	MS-Roc
422	24	33.3	15	8	ADN90308	AdN90308	MS-Roc	495	23	31.9	12	6	ADN90308	AdN90308	MS-Roc
423	24	33.3	15	8	ADN90308	AdN90308	MS-Roc	496	23	31.9	12	6	ADN90308	AdN90308	MS-Roc
424	24	33.3	15	8	ADN90308	AdN90308	MS-Roc	497	23	31.9	12	6	ADN90308	AdN90308	MS-Roc
425	24	33.3	15	8	ADN90308	AdN90308	MS-Roc	498	23	31.9	12	6	ADN90308	AdN90308	MS-Roc
426	24	33.3	15	8	ADN90308	AdN90308	MS-Roc	499	23	31.9	12	6	ADN90308	AdN90308	MS-Roc
427	24	33.3	15	9	ADN90308	AdN90308	MS-Roc	500	23	31.9	12	6	ADN90308	AdN90308	MS-Roc
428	24	33.3	15	10	AEF41957	AeF41957	Human pro	501	23	31.9	12	6	ADN90308	AdN90308	MS-Roc
429	24	33.3	15	10	AEF41957	AeF41957	Human pro	502	23	31.9	12	6	ADN90308	AdN90308	MS-Roc
430	24	33.3	15	10	AEF41957	AeF41957	Human pro	503	23	31.9	12	6	ADN90308	AdN90308	MS-Roc
431	23	31.9	6	5	ABR67283	AbR67283	Human CD6	504	23	31.9	12	6	ADN90308	AdN90308	MS-Roc
432	23	31.9	6	5	ABR67283	AbR67283	Human CD6	505	23	31.9	12	6	ADN90308	AdN90308	MS-Roc
433	23	31.9	7	5	ABR67283	AbR67283	Human CD6	506	23	31.9	12	6	ADN90308	AdN90308	MS-Roc
434	23	31.9	7	5	ABR67283	AbR67283	Human CD6	507	23	31.9	12	6	ADN90308	AdN90308	MS-Roc
435	23	31.9	7	6	ABR67283	AbR67283	Human CD6	508	23	31.9	12	6	ADN90308	AdN90308	MS-Roc
436	23	31.9	7	6	ABR67283	AbR67283	Human CD6	509	23	31.9	12	6	ADN90308	AdN90308	MS-Roc
437	23	31.9	8	5	ABR67283	AbR67283	Human CD6	510	23	31.9	12	6	ADN90308	AdN90308	MS-Roc
438	23	31.9	9	2	AAW9301	AaW9301	Human leu	511	23	31.9	12	6	ADN90308	AdN90308	MS-Roc
439	23	31.9	9	4	ABR83905	AbR83905	Human CD6	512	23	31.9	12	6	ADN90308	AdN90308	MS-Roc
440	23	31.9	9	5	ABR83905	AbR83905	Human CD6	513	23	31.9	12	6	ADN90308	AdN90308	MS-Roc
441	23	31.9	9	8	ADN8142	AdN8142	Human CD6	514	23	31.9	12	6	ADN90308	AdN90308	MS-Roc
442	23	31.9	9	9	ADN8142	AdN8142	Human CD6	515	23	31.9	12	6	ADN90308	AdN90308	MS-Roc
443	23	31.9	9	9	ADN8142	AdN8142	Human CD6	516	23	31.9	12	6	ADN90308	AdN90308	MS-Roc
444	23	31.9	9	9	ADN8142	AdN8142	Human CD6	517	23	31.9	12	6	ADN90308	AdN90308	MS-Roc
445	23	31.9	9	9	ADN8142	AdN8142	Human CD6	518	23	31.9	12	6	ADN90308	AdN90308	MS-Roc
446	23	31.9	10	4	AAW84058	AaW84058	Aradidops	519	23	31.9	12	6	ADN90308	AdN90308	MS-Roc
447	23	31.9	10	4	AAW84058	AaW84058	Aradidops	520	23	31.9	12	6	ADN90308	AdN90308	MS-Roc
448	23	31.9	10	4	AAW84058	AaW84058	Aradidops	521	23	31.9	12	6	ADN90308	AdN90308	MS-Roc
449	23	31.9	10	4	AAW84058	AaW84058	Aradidops	522	23	31.9	12	6	ADN90308	AdN90308	MS-Roc
450	23	31.9	10	5	ABR67271	AbR67271	Human CD6	523	23	31.9	12	6	ADN90308	AdN90308	MS-Roc
451	23	31.9	10	5	ABR67271	AbR67271	Human CD6	524	23	31.9	12	6	ADN90308	AdN90308	MS-Roc
452	23	31.9	10	6	ABR83484	AbR83484	Human car	525	23	31.9	12	6	ADN90308	AdN90308	MS-Roc
453	23	31.9	10	6	ABR83484	AbR83484	Human car	526	23	31.9	12	6	ADN90308	AdN90308	MS-Roc
454	23	31.9	10	7	ADM08987	AdM08987	Canine im	527	23	31.9	12	6	ADN90308	AdN90308	MS-Roc
455	23	31.9	10	7	ADM08987	AdM08987	Canine im	528	23	31.9	12	6	ADN90308	AdN90308	MS-Roc
456	23	31.9	10	8	ADM08987	AdM08987	Canine im	529	23	31.9	12	6	ADN90308	AdN90308	MS-Roc
457	23	31.9	10	8	ADM08987	AdM08987	Canine im	530	23	31.9	12	6	ADN90308	AdN90308	MS-Roc
458	23	31.9	10	8	ADM08987	AdM08987	Canine im	531	23	31.9	12	6	ADN90308	AdN90308	MS-Roc
459	23	31.9	10	9	AEA55659	Aea55659	Human car	532	23	31.9	12	6	ADN90308	AdN90308	MS-Roc
460	23	31.9	10	9	AEA55659	Aea55659	Human car	533	23	31.9	12	6	ADN90308	AdN90308	MS-Roc
461	23	31.9	10	9	AEA55659	Aea55659	Human car	534	23	31.9	12	6	ADN90308	AdN90308	MS-Roc

535	23	31.9	12	6	ADA90872	AdA90872 MS-Roche	608	23	31.9	12	8	ADS94370	AdE94370 Antibody
536	23	31.9	12	6	ADA90749	AdA90749 MS-Roche	609	23	31.9	12	8	ADS94942	AdE94942 Anti-IFN-
537	23	31.9	12	6	ADA91106	AdA91106 MS-R Fab/	610	23	31.9	12	8	ADR69908	AdA69908 Human IL-
538	23	31.9	12	6	ADA91232	AdA91232 MS-R Fab/	611	23	31.9	12	8	ADU81071	AdU81071 MAb G1584
539	23	31.9	12	6	ADA90318	AdA90318 MS-Roche	612	23	31.9	12	9	ADW47133	AdW47133 Anti-CD20
540	23	31.9	12	6	ADA91100	AdA91100 MS-R Fab/	613	23	31.9	12	9	ADM41712	AdM41712 Monoclonal
541	23	31.9	12	6	ADA91103	AdA91103 MS-R Fab/	614	23	31.9	12	9	ADW04979	AdW04979 PAPP-A im
542	23	31.9	12	6	ADA91112	AdA91112 MS-R Fab/	615	23	31.9	12	9	ADX18729	AdX18729 Novel Kin
543	23	31.9	12	6	ADA91238	AdA91238 MS-R Fab/	616	23	31.9	12	9	ADY18779	AdY18779 Novel Kin
544	23	31.9	12	6	ADA90307	AdA90307 MS-Roche	617	23	31.9	12	9	ADY26810	AdY26810 Human ant
545	23	31.9	12	6	ADA90316	AdA90316 MS-Roche	618	23	31.9	12	9	ADY26798	AdY26798 Human ant
546	23	31.9	12	6	ADA90493	AdA90493 MS-Roche	619	23	31.9	12	9	ADY26792	AdY26792 Human ant
547	23	31.9	12	6	ADA90498	AdA90498 MS-Roche	620	23	31.9	12	9	ADY70226	AdY70226 Human Mab
548	23	31.9	12	6	ADA90744	AdA90744 MS-Roche	621	23	31.9	12	9	ADY70232	AdY70232 Human Mab
549	23	31.9	12	6	ADA91016	AdA91016 MS-R Fab/	622	23	31.9	12	9	ADY70856	AdY70856 Human ant
550	23	31.9	12	6	ADA91019	AdA91019 MS-R Fab/	623	23	31.9	12	9	ADZ35810	AdZ35810 Anti-gliuc
551	23	31.9	12	6	ADA90028	AdA90028 Anti-Abet	624	23	31.9	12	9	ADZ35813	AdZ35813 Anti-gliuc
552	23	31.9	12	6	ADA90305	AdA90305 MS-Roche	625	23	31.9	12	9	ADZ35812	AdZ35812 Anti-gliuc
553	23	31.9	12	6	ADA90312	AdA90312 MS-Roche	626	23	31.9	12	9	ADZ35814	AdZ35814 Anti-gliuc
554	23	31.9	12	6	ADA90491	AdA90491 MS-Roche	627	23	31.9	12	9	AEA18878	AEa18878 Antino aci
555	23	31.9	12	6	ADA90496	AdA90496 MS-Roche	628	23	31.9	12	9	AEA53691	AEa53691 Novel hum
556	23	31.9	12	6	ADA90748	AdA90748 MS-Roche	629	23	31.9	12	9	AEA45346	AEa45346 Apolipopr
557	23	31.9	12	6	ADA90750	AdA90750 MS-Roche	630	23	31.9	12	9	AEA45856	AEa45856 Apolipopr
558	23	31.9	12	6	ADA90868	AdA90868 MS-Roche	631	23	31.9	12	9	AEA24217	AEa24217 Anti-HAaH
559	23	31.9	12	6	ADA91223	AdA91223 MS-R Fab/	632	23	31.9	12	9	AEBO1033	AEb01033 Human IPI
560	23	31.9	12	6	ADA90300	AdA90300 MS-Roche	633	23	31.9	12	9	AEBO1027	AEb01027 Human IPI
561	23	31.9	12	6	ADA90327	AdA90327 MS-Roche	634	23	31.9	12	9	AEBO1025	AEb01025 Human IPI
562	23	31.9	12	6	ADA90625	AdA90625 MS-Roche	635	23	31.9	12	9	AEBO1032	AEb01032 Human IPI
563	23	31.9	12	6	ADA90303	AdA90303 MS-Roche	636	23	31.9	12	9	AEBS2752	AEb2752 Sma11 hRA
564	23	31.9	12	6	ADA90480	AdA90480 MS-Roche	637	23	31.9	12	9	AEBO0612	AEb00612 Phosphata
565	23	31.9	12	6	ADA90489	AdA90489 MS-Roche	638	23	31.9	12	9	AEBO0562	AEb00562 Serine/Th
566	23	31.9	12	6	ADA90494	AdA90494 MS-Roche	639	23	31.9	12	9	AEED87304	AEe87304 Fv2A7 lig
567	23	31.9	12	6	ADA90633	AdA90633 MS-Roche	640	23	31.9	12	10	AEBO3767	AEe03767 Antibody
568	23	31.9	12	6	ADA90866	AdA90866 MS-Roche	641	23	31.9	12	10	AEBO3765	AEe03765 Phox-spec
569	23	31.9	12	6	ADA91013	AdA91013 MS-R Fab/	642	23	31.9	12	10	AEBO3736	AEe03736 Phox-spec
570	23	31.9	12	6	ADA91109	AdA91109 MS-R Fab/	643	23	31.9	12	10	AEBO3737	AEe03737 Phox-spec
571	23	31.9	12	6	ADA90304	AdA90304 MS-Roche	644	23	31.9	12	10	AEBO3731	AEe03731 Phox-spec
572	23	31.9	12	6	ADA90478	AdA90478 MS-Roche	645	23	31.9	12	10	AEBO37380	AEe037380 Phox-spec
573	23	31.9	12	6	ADA90482	AdA90482 MS-Roche	646	23	31.9	12	10	AEBO37374	AEe037374 Phox-spec
574	23	31.9	12	6	ADA90483	AdA90483 MS-Roche	647	23	31.9	12	10	AEBO37359	AEe037359 Phox-spec
575	23	31.9	12	6	ADA90629	AdA90629 MS-Roche	648	23	31.9	12	10	AEBO37368	AEe037368 Phox-spec
576	23	31.9	12	6	ADA90630	AdA90630 MS-Roche	649	23	31.9	12	10	AEBO37694	AEe037694 Antibody
577	23	31.9	12	6	ADA90639	AdA90639 MS-Roche	650	23	31.9	12	10	AEF24380	AEf24380 Mouse PAN
578	23	31.9	12	6	ADA90753	AdA90753 MS-Roche	651	23	31.9	12	10	AEF11066	AEf11066 Human c10
579	23	31.9	12	6	ADA90319	AdA90319 MS-Roche	652	23	31.9	12	10	AEF73689	AEf73689 Human IL-
580	23	31.9	12	6	ADA90326	AdA90326 MS-Roche	653	23	31.9	12	10	AEBO0330	AEg00330 Kalikirel
581	23	31.9	12	6	ADA90481	AdA90481 MS-Roche	654	23	31.9	12	10	AEBO0678	AEg00678 Kalikirel
582	23	31.9	12	6	ADA90627	AdA90627 MS-Roche	655	23	31.9	12	10	AEBO0492	AEg00492 Kalikirel
583	23	31.9	12	6	ADA90754	AdA90754 MS-Roche	656	23	31.9	12	10	AEBO0432	AEg00432 Kalikirel
584	23	31.9	12	6	ADA90755	AdA90755 MS-Roche	657	23	31.9	12	10	AEBO0324	AEg00324 Kalikirel
585	23	31.9	12	6	ADA91115	AdA91115 MS-R Fab/	658	23	31.9	12	10	AEBO1062	AEg01062 Kalikirel
586	23	31.9	12	6	ADA91226	AdA91226 MS-R Fab/	659	23	31.9	12	10	AEBO1134	AEg01134 Kalikirel
587	23	31.9	12	6	ADA91229	AdA91229 MS-R Fab/	660	23	31.9	12	10	AEBO0774	AEg00774 Kalikirel
588	23	31.9	12	6	ADA91229	AdA91229 MS-R Fab/	661	23	31.9	12	10	AEBO0606	AEg00606 Kalikirel
589	23	31.9	12	6	ADA90096	AdA90096 Anti-Abet	662	23	31.9	12	10	AEBO0750	AEg00750 Kalikirel
590	23	31.9	12	6	ADA90314	AdA90314 MS-Roche	663	23	31.9	12	10	AEBO0456	AEg00456 Kalikirel
591	23	31.9	12	6	ADA90632	AdA90632 MS-Roche	664	23	31.9	12	10	AEBO0660	AEg00660 Kalikirel
592	23	31.9	12	6	ADA90752	AdA90752 MS-Roche	665	23	31.9	12	10	AEBO0660	AEg00660 Kalikirel
593	23	31.9	12	7	ABO33866	ABO33866 Anti-GPI-	666	23	31.9	13	4	AAU10755	AAu10755 Target ep
594	23	31.9	12	7	ABO33864	ABO33864 Anti-GPI-	667	23	31.9	13	5	ABR74392	ABr74392 Karyophi1
595	23	31.9	12	7	ABO33867	ABO33867 Anti-GPI-	668	23	31.9	13	6	ABJ18710	ABj18710 Antibody
596	23	31.9	12	7	ABO33868	ABO33868 Anti-GPI-	669	23	31.9	13	6	ABJ18704	ABj18704 Antibody
597	23	31.9	12	7	ADCA4337	ADc44337 Endotheli	670	23	31.9	13	6	ABJ18712	ABj18712 Antibody
598	23	31.9	12	7	ADCA4053	ADd40553 3E1/4G11	671	23	31.9	13	6	ABJ18714	ABj18714 Antibody
599	23	31.9	12	8	ADL17447	ADl17447 Human MUP	672	23	31.9	13	7	ADM75108	Adm75108 Potential
600	23	31.9	12	8	ADDE25805	ADj25805 Anti-alph	673	23	31.9	13	7	ADM75088	Adm75088 Potential
601	23	31.9	12	8	ADU25666	ADj25666 Mouse aPC	674	23	31.9	13	7	ADM74843	Adm74843 Potential
602	23	31.9	12	8	ADL93535	ADl93535 Human CD4	675	23	31.9	13	9	AECC0623	AEc00623 Serine/Th
603	23	31.9	12	8	ADOA42771	ADo42771 Leader se	676	23	31.9	13	9	AECC0626	AEc00626 Phosphata
604	23	31.9	12	8	ADOC39455	ADo39455 Novel hum	677	23	31.9	14	2	AAAR11031	AAr11031 Human gam
605	23	31.9	12	8	ADPA47243	ADp47243 Human pho	678	23	31.9	14	4	AAAR33230	AAr33230 HIV-Va748
606	23	31.9	12	8	ADPA47279	ADp47279 Human pho	679	23	31.9	14	4	AAAR7564	AAr7564 Human pep
607	23	31.9	12	8	ADPA47231	ADp47231 Human pho	680	23	31.9	14	4	AAAR7986	AAr7986 Human pep
					ADs87945	ADs87945 Anti-IFN-						AAAR6809	AAr6809 Human pep

681	23	31.9	14	4	AAB92233	Aab92233	Toxin pep
682	23	31.9	14	4	AAB88163	Aab88163	CD66 pep
683	23	31.9	14	6	ADA19583	Ada19583	Carclnoem
684	23	31.9	14	8	ADU48708	Adu48708	Human int
685	23	31.9	14	9	AED80969	Aed80969	Vespa ori
686	23	31.9	15	1	AAEP82830	Aap82830	Non-A, No
687	23	31.9	15	2	AAAR14336	Aair14336	Sciavo pe
688	23	31.9	15	2	AAAR14397	Aair14397	Sciavo pe
689	23	31.9	15	2	AAAR62572	Aair62572	Human hep
690	23	31.9	15	2	AAAR24979	Aair24979	Peptide e
691	23	31.9	15	2	AAAR29487	Aair29487	Peptide #
692	23	31.9	15	2	AAAR4051	Aair4051	Histone H
693	23	31.9	15	2	AAAR73220	Aair73220	ATF1 epit
694	23	31.9	15	2	AAAR73425	Aair73425	Human sec
695	23	31.9	15	2	AAAR57349	Aair57349	Human his
696	23	31.9	15	3	AAAR65813	Aair65813	FADD-homo
697	23	31.9	15	4	ABBI12911	Abbi12911	Human C35
698	23	31.9	15	4	ABBI12870	Abbi12870	Human C35
699	23	31.9	15	4	ABBI12831	Abbi12831	Human C35
700	23	31.9	15	4	ABBI12923	Abbi12923	Human C35
701	23	31.9	15	4	AAAG64562	Aag64562	Human myo
702	23	31.9	15	4	ABP24487	Abp24487	HIV DR su
703	23	31.9	15	4	ABP24431	Abp24431	HIV DR su
704	23	31.9	15	5	ABPE58713	Abp58713	Human fib
705	23	31.9	15	6	ABR337229	Abj37229	Rhodopsin
706	23	31.9	15	6	ABR33632	Abj33632	Human can
707	23	31.9	15	6	ABR33636	Abj33636	Human can
708	23	31.9	15	6	ABR33718	Abj33718	Human can
709	23	31.9	15	6	ABR33684	Abj33684	Human can
710	23	31.9	15	6	ABR33746	Abj33746	Human can
711	23	31.9	15	6	ABR33668	Abj33668	Human can
712	23	31.9	15	6	ABR33765	Abj33765	Human can
713	23	31.9	15	6	ABR33619	Abj33619	Human can
714	23	31.9	15	6	ABR33766	Abj33766	Human can
715	23	31.9	15	7	ADCS4047	Adc4047	Human reg
716	23	31.9	15	7	ADLC00354	Adl00354	Polypept
717	23	31.9	15	8	ADLI14271	Adl14271	Immunogen
718	23	31.9	15	8	ADN71512	Adn71512	Human 273
719	23	31.9	15	8	ADN70546	Adn70546	Human 273
720	23	31.9	15	8	ADN65099	Adn65099	HLA bindi
721	23	31.9	15	8	ADN65098	Adn65098	HLA bindi
722	23	31.9	15	8	ADN65110	Adn65110	HLA bindi
723	23	31.9	15	8	ADN65280	Adn65280	HLA bindi
724	23	31.9	15	8	ADN05702	Adn05702	Antipsori
725	23	31.9	15	8	ADN047146	Ado47146	Antio aci
726	23	31.9	15	8	ADP26479	Adp26479	Plasmodiu
727	23	31.9	15	8	ADSI13553	Adsi13553	Human rne
728	23	31.9	15	8	ADT07826	Adt07826	Human int
729	23	31.9	15	8	ADM15936	Adm15936	Human act
730	23	31.9	15	9	ADV44318	Adv44318	Human Hdm
731	23	31.9	15	9	ADV91487	Adv91487	Human Gas
732	23	31.9	15	9	ADV21599	Adv21599	SIV gag p
733	23	31.9	15	9	ADV22686	Adv22686	HIV-1 Vif
734	23	31.9	15	9	ADV70545	Adv70545	Bovine pa
735	23	31.9	15	9	ADM12731	Adm12731	HIV-1 gp1
736	23	31.9	15	9	ADY71996	Ady71996	Human imm
737	23	31.9	15	9	ADZ69811	Adz69811	Botulinum
738	23	31.9	15	9	ADZ69739	Adz69739	Botulinum
739	23	31.9	15	9	ADZ69754	Adz69754	Botulinum
740	23	31.9	15	9	AEC23563	Aec23563	Human c-S
741	23	31.9	15	9	AEC98732	Aec98732	HLA-DR bi
742	23	31.9	15	9	AEC98815	Aec98815	HLA-DR bi
743	23	31.9	15	9	AEC98731	Aec98731	HLA-DR bi
744	23	30.6	5	5	ABPE7301	Abpe7301	Human CD6
745	23	30.6	5	7	ADJ82687	Adj82687	Shuffled
746	23	30.6	6	8	ADU08263	Adu08263	Heat shoc
747	23	30.6	7	2	AAAY14775	Aay14775	P450 enzy
748	23	30.6	7	2	ADP79638	Adp79638	Parapoxvi
749	23	30.6	7	8	ADP75039	Adp75039	Parapoxvi
750	23	30.6	7	8	ADX85702	Adx85702	Epitope f
751	23	30.6	8	7	ADT62401	Adt62401	Tryptic m
752	22	30.6	8	8	ADO22334	Ado22334	Cyclin/cd
753	22	30.6	8	8			

RESULT 1
ADV91451
ID ADV91451 standard, peptide, 15 AA.
AC ADV91451;
XX
DT 10-MAR-2005 (first entry)
XX
DE Human growth arrest specific gene 6 (Ga6) G domain peptide #1.
XX
KW Growth arrest specific gene 6; Ga6; cardiovascular disease; cancer;
KW atherosclerosis; sepsis; glomerulosclerosis; diabetes;
KW rheumatoid arthritis; HIV infection; osteoarthritis; osteoporosis;
KW multiple sclerosis; cardiovascular-gen.; antirheumatic; antithrombotic;
KW anti-HIV; cytostatic; neuroprotective; thrombolytic; cardiac;
KW cerebroprotective; vasotropic; antitextile; osteopathic;
KW immunosuppressive; nephrotropic; antidiabetic; osteopathic;
KW antibody production.
OS Homo sapiens.
XX

ALIGNMENTS
Aab11479 Enterococ
Aar99370 Cw6 conse
Aau27018 Human Leu
Aau66685 Human Leu
Abp11572 HIV A01 s
Abp15318 HIV A24 s
Abp18459 HIV B62 s
Abu08168 MART-1 57
Adb39044 Human tum
Adb30074 HIV bindi
Ade88256 Immunogen
Ade88264 Immunogen
Adne4502 HLA bindi
Adne4297 HLA bindi
Adne4392 HLA bindi
Adp25766 Plasmodiu
Adt11377 HLA-A2.1
Adt11363 HLA-A2.1
Adr90432 Melanoma-
Adr90463 Melanoma-
Adr44516 BIR domai
Adr44547 BIR domai
Adp80118 Human HLA
Adt40420 HSARS vlr
Adt579837 HSARS vlr
Adt37950 HSARS vlr
Aee67308 Cancer tr
Aee63125 ML-TAP (1
Aab13857 Influenza
Abb14114 Human C35
Abp17615 HIV B58 s
Abp11596 HIV A01 s
Aau10525 Human leu
Abro05416 Human can
Abj71942 P. papara
Ada49582 Multi-epi
Adk40055 PVA molec
Adk40051 PVA molec
Adk40046 PVA molec
Adk40044 PVA molec
Adt31708 Tumour an
Adm12002 Chemokine
Adm11339 Chemokine
Ado24260 P falcipa
Adz40762 Multi-epi
Aec67334 Human 109
Aab2860 Human p53

PN WO2004108748-A2.
XX
PD 16-DEC-2004.
XX
PF 24-SEP-2003; 2003WO-US029909.
XX
PR 24-SEP-2002; 2002US-0413250P.
XX
PA (CENZ) CENTOCOR INC.
XX
PI Yang J, Heavner G, Jordan R, Sweet RW;
DR WPI; 2005-031655/03.
XX
PT Novel human growth arrest specific polypeptide-6, useful for generating
PT antibodies against growth arrest specific polypeptide-6, and for treating
PT cardiovascular, rheumatoid arthritis, HIV infection, leukemia, multiple
PT sclerosis.
XX
XX Claim 1; SEQ ID NO 2; 107pp; English.
XX
CC The invention relates to an isolated human growth arrest specific gene 6
CC (Gas6) polypeptide. The invention also relates to a recombinant DNA
CC molecule encoding the polypeptide, an antibody or antigen binding
CC fragment capable of binding to the polypeptide and a labeled antibody
CC generated against Gas6. The Gas6 polypeptide is useful for generating
CC antibodies against Gas6, which involves immunization with the polypeptide
CC or screening recombinant antibodies with the polypeptide. The antibodies
CC are useful for detecting Gas6 polypeptide in a sample suspected of
CC containing Gas6. Compositions containing the polypeptide are useful for
CC preventing or treating cardiovascular diseases resulting from a
CC dysfunction in a mammal. The compositions are also useful for treating
CC cancer, atherosclerosis, sepsis, glomerulosclerosis, diabetes, rheumatoid
CC arthritis, HIV infection, osteoarthritis, osteoporosis and multiple
CC sclerosis. This sequence represents a human Gas6 G domain peptide of the
CC invention.
XX
SQ Sequence 15 AA;
XX
Query Match 100.0%; Score 72; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 VPFSVAKSVKSLYLIG 15
Db 1 VPFSVAKSVKSLYLIG 15
XX
RESULT 2
AA17975
ID AA17975 standard; peptide; 12 AA.
XX
AC AA17975;
XX
DT 04-AUG-1999 (first entry)
XX
DE Peptide Seq ID No: 6 of JP11127869.
XX
KM Hexulose phosphate isomerase; enzyme; recombinant; M. gastri.
XX
XX Mycobacterium gastri.
XX
XX OS JP11127869-A.
XX
XX PN 18-MAY-1999.
XX
PD 09-JUL-1998; 98JP-00194808.
XX
PF 28-AUG-1997; 97JP-00233131.
XX
PR (AJIN) AJINOMOTO KK.
XX
PA Kato N;
XX
PI

XX
DR WPI; 1999-350329/30.
XX
XX
PT New hexulose phosphate isomerase gene - prepared recombinantly with high
PT efficiency.
XX
XX Example; Page 6; 19pp; Japanese.
XX
CC The invention relates to a Mycobacterium gastri hexulose phosphate
CC isomerase. The enzyme can be produced recombinantly by culturing a cell
CC which is transformed with a DNA coding for hexulose phosphate isomerase
CC and collecting the enzyme from the culture
XX
SQ Sequence 12 AA;
XX
Query Match 50.0%; Score 36; DB 2; Length 12;
Best Local Similarity 80.0%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1 VPFSVAKSVK 10
Db 3 VPFSVAGGVK 12
XX
RESULT 3
ADW47130
ID ADW47130 standard; peptide; 12 AA.
XX
AC ADW47130;
XX
DT 24-MAR-2005 (first entry)
XX
DE Anti-CD20 monoclonal antibody light chain MHB20-2,14 CDR 1.
XX
XX CD20; monoclonal antibody; rheumatoid arthritis; antiarthritic;
KM antirheumatic; immune disorder; inflammation; musculoskeletal disease;
KM idiopathic thrombocytopenic purpura; hemostatic; hemolytic anemia.
XX
XX Mus musculus.
OS
XX
XX WO200500901-A2.
FN
PD 06-JAN-2005.
XX
PE 07-MAY-2004; 2004WO-US014326.
XX
XX 09-MAY-2003; 2003US-0469451P.
PR
XX (UYDU-) UNIV DUKE.
PA
PI Tedder TF, Uchida J, Hamaguchi Y, Poe JC;
XX
XX WPI; 2005-066556/07.
XX
DR
XX
PT Novel monoclonal antibody (mAb) binding to CD20 or mouse CD20, in which
PT density of binding of mAb to B cells is two-fold higher than density of
PT binding of mAb1F5 to B cells, useful for depleting B cells, and treating
PT B cell disorder.
XX
XX Example 1; SEQ ID NO 89; 205pp; English.
XX
CC The invention relates to a monoclonal antibody (mAb) or its antigen-
CC binding fragment that specifically binds to human CD20 or mouse CD20,
CC where the density of binding of mAb or antigen-binding fragment to B
CC cells is at least two-fold higher than the density of binding of mAb 1F5
CC to B cells. Also included are a pharmaceutical composition comprising mAb
CC in a carrier, a pharmaceutical composition (comprising mAb or its antigen
CC binding fragment which specifically binds to the same antigenic
CC determinant as a monoclonal antibody chosen from HB20-1, HB20-3, HB20-4
CC and HB20-25 in a carrier), a cell line producing the mAb, producing the
CC mAb, an antigen binding fragment of the mAb, an isolated nucleic acid
CC encoding a heavy chain or light chain comprising a variable region
CC (comprising CDR3, or CDR1, CDR2 and CDR3 regions from mAb chosen from

CC HB20-1, HB20-3, HB20-4, HB20-5, HB20-25, MB20-11, MB20-1, MB20-2, MB20-7,
CC MB20-8, MB20-10, MB20-11, MB20-14, MB20-16 and MB20-18), a vector
CC comprising the nucleic acid, a cell comprising the nucleic acid or
CC vector, and depleting B cells in a mammalian subject (involving
CC administering the mAb and anti-CD22 or anti-CD19 antibody). The anti-CD20
CC mAb, compositions and cells are useful for depleting B cells in a
CC mammalian subject and for treating a B cell disorder. The B cell disorder
CC is B cell malignancy or autoimmune disease e.g. Rheumatoid arthritis,
CC idiopathic thrombocytopenic purpura or hemolytic anemia. The mammalian
CC subject is resistant to anti-CD20 mAb therapy or resistant to therapy
CC with mAb C2B8. The mammalian subject has been or is currently treated
CC with chemotherapy. The mammalian subject had a relapse in a B cell
CC disorder. The mammalian subject is immunocompromised. The present
CC sequence represents a CDR (complementarity determining region) from anti-
CC CD20 monoclonal antibody.
CC
XX
SQ Sequence 12 AA;

Query Match 41.7%; Score 30; DB 9; Length 12;
Best Local Similarity 54.5%; Pred. No. 2.2e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 4 SVAKSVKSLYL 14
||:|:|:|
Db 1 SVSSSIRSNYL 11

RESULT 4
AEA46220
ID AEA46220 standard; peptide; 12 AA.
XX
AC AEA46220;
XX
DT 11-AUG-2005 (first entry)
XX
DE Apolipoprotein E C-terminal domain antibody VL-CDRI peptide #118.
XX
XX Neuroprotective; Nootropic; Antidiabetic; Endocrine-Gen.; Nephrotropic;
XX Antiparkinsonian; Anticonvulsant; Respiratory-Gen; Apolipoprotein E;
XX Alzheimer's disease; amyloidosis; Parkinson's disease; Huntingtons chorea;
XX Kuru; Dementia; non-insulin dependent diabetes; Down syndrome;
XX Spongiform encephalopathy; Creutzfeldt Jakob disease;
XX motor neurone disease; chronic obstructive pulmonary disease.
XX
OS Homo sapiens.
XX
XX GB2408508-A.
XX
XX 01-JUN-2005.
XX
XX 26-NOV-2004; 2004GB-00026043.
XX
XX 28-NOV-2003; 2003US-0525174P.
XX
XX (ASTR) ASTRAZENEGA AB.
XX PA (DVAX-) DVAX CORP.
XX
XX Nordstedt C, Goldschmidt T, Hendriks M, Hoet R, Hoogenboom H;
XX Hufon S, Andersson CV, Lindquist J, Sunemark D, Leonov S;
XX
XX WPI; 2005-408785/42.
XX
XX
XX New human antibody or antibody fragment which binds to a sequence of the
XX C-terminal domain of Apolipoprotein E (ApoE-CTD), useful for
XX manufacturing a medicament for treating or preventing an amyloid disorder
XX e.g. Alzheimers disease.
XX
XX Example 23; Page 113; 392pp; English.
XX
XX The present invention relates to a human antibody or antibody fragment,
XX which binds to the C-terminal domain of Apolipoprotein E (ApoE-CTD),
XX AEA44803) and also to human plaques. The antibody or its fragment is
XX useful for manufacturing a medicament for treating or preventing an

CC amyloid disorder such as Alzheimers disease, primary systemic
CC amyloidosis, secondary systemic amyloidosis, senile systemic amyloidosis,
CC familial amyloid polynuropathy I, familial amyloid polynuropathy III,
CC familial non-neuropathic amyloidosis, hereditary cerebral amyloid
CC angiopathy, Familial British Dementia, Hemodialysis-related amyloidosis,
CC Familial amyloidosis (Finnish type), Familial subepithelial corneal
CC amyloid, type II diabetes, Hereditary renal amyloidosis, Pituitary-gland
CC thyroid, Atrial amyloidosis, Familial Danish dementia (FDD), Downs
CC syndrome, Spongiform encephalopathies, Sporadic Creutzfeldt-Jakob
CC disease, Gerstmann-Strausler-Scheinker Disease (GSS), Kuru, Parkinsons
CC disease, Huntingtons disease, Familial amyotrophic lateral sclerosis, and
CC chronic obstructive pulmonary disease. The present sequence was used to
CC illustrate the invention.
CC
XX
SQ Sequence 12 AA;

Query Match 41.7%; Score 30; DB 9; Length 12;
Best Local Similarity 63.6%; Pred. No. 2.2e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 4 SVAKSVKSLYL 14
||:|:|:|
Db 1 SVGSVSSNLY 11

RESULT 5
ADM12121
ID ADM12121 standard; peptide; 9 AA.
XX
XX ADM12121;
XX
XX 07-APR-2005 (first entry)
XX
XX
XX Human CD20 antigen peptide, SEQ ID No:219.
XX
XX
XX Leukemic antigen; antigen; CD20; cytotoxic T-lymphocyte;
XX Immune stimulation; pharmaceutical; vaccine; cancer; cytostatic.
XX
XX OS Homo sapiens.
XX
XX PN MO2005007673-A2.
XX
XX 27-JAN-2005.
XX
XX 02-JUL-2004; 2004WO-US021510.
XX
XX 03-JUL-2003; 2003US-0484689P.
XX
XX (UYRU-) UNIV RUSH MEDICAL CENT.
XX
XX Bae J;
XX
XX WPI; 2005-102081/11.
XX
XX
XX New leukemic antigen comprising a fragment of CD19 or CD20 antigen, or
XX its variant or homolog, that is capable of stimulating a cytotoxic T-
XX lymphocyte reaction, useful for diagnosing, preventing or treating
XX diseases such as cancer.
XX
XX Example 1; SEQ ID NO 219; 69pp; English.
XX
XX
XX The invention relates to isolated leukemic antigens comprising a fragment
XX of CD19 or CD20 antigen, or its mammalian homolog or variant that is
XX capable of stimulating a cytotoxic T-lymphocyte reaction. The fragment or
XX its variant is 8-80 amino acids in length, and the isolated leukemic
XX antigen is not a 44 amino acid extracellular domain of CD20. Also
XX described are (i) a method of stimulating an immune effector cell
XX response, (ii) an immune effector cell produced by the above method,
XX (iii) an antigen presenting cell produced by contacting the isolated
XX leukemic antigen cited above with an antigen presenting cell, (iv) an
XX isolated nucleic acid that encodes the above isolated leukemic antigen,
XX (v) a pharmaceutical composition comprising the isolated leukemic antigen

CC and a pharmaceutical carrier, and (v1) an antibody, or its functional
CC fragment, that is capable of binding the above isolated leukemic antigen.
CC The isolated leukemic antigen comprises any of SEQ ID NOS: 1-12 given in
CC the specification, or their variant having one or more conservative or
CC non-conservative amino acid substitutions. The leukemic antigens can be
CC included in a pharmaceutical composition such as a cancer vaccine. The
CC compositions and methods of the invention are useful for stimulating an
CC immune response against diseases such as cancer, or for diagnosing or
CC treating cancer. This sequence represents a CD20 antigen peptide tested
CC as a possible immunogenic epitope.

XX Sequence 9 AA:

Query Match 40.3%; Score 29; DB 9; Length 9;
Best Local Similarity 62.5%; Pred. No. 2,1e+06;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 SVKSLVYG 15
|::|::|
Db 1 SIQSLFLG 8

RESULT 6

ID ADK40054 standard; peptide; 10 AA.

XX ADK40054;

DT 06-MAY-2004 (first entry)

DE PNA molecule-related transporter peptide #226.

XX modified peptide nucleic acid; PNA; TP-L-PNA; TP; transporter peptide; L;
KM bond; linker; antibacterial; antimicrobial; cytostatic; virucide;
KM immunosuppressive; antisense-therapy; infectious disease;
KM bacterial infection; disinfection; cancer; bacterial; viral infection;
KM metabolic disease; immunological disorder.

XX Unidentified.

XX WO2003092736-A2.

XX 13-NOV-2003.

PF 01-MAY-2003; 2003WO-DK000280.

PR 01-MAY-2002; 2002DK-00000661.

PA (PANT-) PANTHECO AS.

PI Tolborg J, Frandsen TP, Nielsen BR, Johansen C, Kjaerulf S;

XX WPI; 2004-011826/01.

PT New modified peptide nucleic acid (PNA) molecule, useful in treating
PT and/or preventing cancer, viral infections, metabolic diseases,
PT immunological disorders, and in particular bacterial infections.

PS Claim 6; Page 84; 96pp; English.

XX This invention relates to a novel modified peptide nucleic acid (PNA)
CC molecule. The invention comprises TP-L-PNA where TP transporter peptide;
CC L bond or a linker; PNA an oligomer of 4-35 monomers. The invention may
CC be useful for the development of compounds with an antibacterial,
CC anticicrobial, cytostatic, virucide or immunosuppressive. In addition,
CC the disclosed sequences could be used for antisense-therapy. The
CC compounds of the PNA molecule are useful in medicine, in particular for
CC the inactivation of the expression of specific genes by targeting the
CC genes at the mRNA, rRNA or DNA level. The PNA sequence is useful in the
CC treatment and/or prevention of infectious diseases, particularly
CC bacterial infections, or in disinfection of non-living objects. The
CC methods and compositions of the present invention are also useful for
CC treating cancer, bacterial and viral infections, metabolic diseases and

CC immunological disorders. The present sequence is that of a transporter
CC peptide which may be used during the creation of a PNA molecule of the
CC invention.

XX Sequence 10 AA;

Query Match 40.3%; Score 29; DB 8; Length 10;
Best Local Similarity 75.0%; Pred. No. 2,8e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 FSVAKSVK 10
|::|::|
Db 3 FKVAKAVK 10

RESULT 7

ID ADU08556 standard; peptide; 7 AA.

XX ADU08556;

DT 13-JAN-2005 (first entry)

DE Heat shock protein binding peptide #85.

XX Hybrid antigen; antigenic domain; infectious agent; tumour antigen;
KM binding domain; heat shock protein; hsp; immune response;
KM infectious disease; cancer; cytostatic; antimicrobial; immunostimulant.

XX Unidentified.

PN WO2004091493-A2.

XX 28-OCT-2004.

PF 09-APR-2004; 2004WO-US010983.

PR 11-APR-2003; 2003US-0462469P.

PR 18-APR-2003; 2003US-0463746P.

PR 16-SEP-2003; 2003US-0503417P.

PR 12-FEB-2004; 2004US-00776521.

PR 13-FEB-2004; 2004WO-US004340.

PR 08-APR-2004; 2004US-00820067.

PA (MOJA-) MOJAVE THERAPEUTICS INC.

PI Flechtner JB, Prince-Cohane K, Mehta S, Slusaregicz P, Andjelic S;

XX Barber BH;

XX WPI; 2004-775516/76.

PT Hybrid antigen useful for treating an infectious disease or cancer,

PT comprises an antigenic domain from the infectious agent or cancer joined

PT to a heat shock protein binding domain through an improved linker

PT peptide.

PS Disclosure; Page 32; 99pp; English.

XX The invention relates to hybrid antigens comprising at least one
CC antigenic domain of an infectious agent or tumour antigen, at least one
CC binding domain that non-covalently binds to a heat shock protein (hsp),
CC and at least one peptide linker between them. Also disclosed are: (a) a
CC composition for inducing an immune response to an infectious agent or
CC tumour antigen comprising at least one of the hybrid antigens or a
CC complex of at least one heat shock protein and at least one of the hybrid
CC antigens, (b) a method for inducing an immune response to an infectious
CC agent or tumour antigen by administering a hybrid antigen and a heat
CC shock protein, where the hybrid antigen and the heat shock protein are
CC non-covalently bound, and (c) treating an infectious disease or cancer by
CC administering a hybrid antigen and a heat shock protein. The heat shock
CC protein is preferably hsp70. The composition is administered via oral or
CC parenteral route. The hybrid antigen is useful in preparing a composition
CC for treating or preventing cancer or infectious disease. The new peptide

CC linkers give the antigens improved activity. Note: Many of the SEQ ID Nos
CC are replicated more than once in the specification but the sequences of
CC these replicated SEQ ID Nos are not the same. This sequence represents a
CC heat shock protein binding sequence.
XX

SQ Sequence 7 AA;

Query Match 38.9%; Score 28; DB 8; Length 7;
Best Local Similarity 71.4%; Pred. No. 2.1e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 9 VKSLYIG 15
Db 1 VKKLYIG 7

RESULT 8
ADU89525
ID ADU89525 standard; peptide; 8 AA.
XX
AC ADU89525;
XX
XX 18-NOV-2004 (first entry)
XX
DE Novel hybrid antigen-related peptide SegID315.
XX
XX hybrid antigen; antigenic domain; infectious agent; tumour antigen;
KW binding domain; heat shock protein; antimicrobial; cytostatic; vaccine;
KW gene therapy; infectious disease; cancer.
XX
OS unidentified.
XX
XX WO2004071457-A2.
XX
XX 26-AUG-2004.
XX
XX 13-FEB-2004; 2004WO-US004340.
XX
XX 13-FEB-2003; 2003US-0447142P.
XX
XX 11-APR-2003; 2003US-0462469P.
XX
XX 18-APR-2003; 2003US-0463746P.
XX
XX 16-SEP-2003; 2003US-0503417P.
XX
XX 12-FEB-2004; 2004US-00776521.
XX
XX (MOA-) MOJAVE THERAPEUTICS INC.
XX
XX PA Fletcher J, Prince-Cohane K, Mehra S, Slusarewicz P, Andjelic S;
XX PI Barber B;
XX
XX WPI; 2004-625768/60.
XX
XX

PT New hybrid antigens comprising an antigenic domain and improved heat
PT shock protein-binding domains, useful for preventing or treating
PT infectious diseases or cancer.
XX
XX
XX Disclosure; SEQ ID NO 315; 56pp; English.
XX

CC This invention relates to a novel hybrid antigen which comprises at least
CC one antigenic domain of an infectious agent or tumour antigen and a
CC binding domain that non-covalently binds to a heat shock protein. The
CC invention may be useful for the production of compounds with an
CC antimicrobial or cytostatic activity. In addition, the invention may
CC prove useful for the production of a vaccine or for gene therapy. The
CC composition and methods disclosed are useful for preventing or treating
CC infectious diseases or cancer. The present sequence is that of a heat
CC shock protein binding domain peptide which was used in the
CC exemplification of the invention.
XX
XX

SQ Sequence 8 AA;

Query Match 38.9%; Score 28; DB 8; Length 8;
Best Local Similarity 71.4%; Pred. No. 2.1e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 VKSLYIG 15
Db 1 VKKLYIG 7

RESULT 9
ADU08445
ID ADU08445 standard; peptide; 8 AA.
XX
AC ADU08445;
XX
XX 13-JAN-2005 (first entry)
XX
XX
DE Heat shock protein binding domain #195.
XX
XX
XX Hybrid antigen; antigenic domain; infectious agent; tumour antigen;
KW binding domain; heat shock protein; hsp; immune response;
KW infectious disease; cancer; cytostatic; antimicrobial; immunostimulant.
XX
OS unidentified.
XX
XX WO2004091493-A2.
XX
XX 28-OCT-2004.
XX
XX 09-APR-2004; 2004WO-US010983.
XX
XX 11-APR-2003; 2003US-0462469P.
XX
XX 18-APR-2003; 2003US-0463746P.
XX
XX 16-SEP-2003; 2003US-0503417P.
XX
XX 12-FEB-2004; 2004US-00776521.
XX
XX 13-FEB-2004; 2004WO-US004340.
XX
XX 08-APR-2004; 2004US-00820067.
XX
XX (MOA-) MOJAVE THERAPEUTICS INC.
XX
XX PA Fletcher JB, Prince-Cohane K, Mehra S, Slusarewicz P, Andjelic S;
XX PI Barber BH;
XX
XX WPI; 2004-775516/76.
XX
XX

PT Hybrid antigen useful for treating an infectious disease or cancer;
PT comprises an antigenic domain from the infectious agent or cancer joined
PT to a heat shock protein binding domain through an improved linker
PT peptide.
XX
XX
XX Disclosure; Page 42; 99pp; English.
XX

CC The invention relates to hybrid antigens comprising at least one
CC antigenic domain of an infectious agent or tumour antigen, at least one
CC binding domain that non-covalently binds to a heat shock protein (hsp),
CC and at least one peptide linker between them. Also disclosed are: (a) a
CC composition for inducing an immune response to an infectious agent or
CC tumour antigen comprising at least one of the hybrid antigens or a
CC complex of at least one heat shock protein and at least one of the hybrid
CC antigens, (b) a method for inducing an immune response to an infectious
CC agent or tumour antigen by administering a hybrid antigen and a heat
CC shock protein, where the hybrid antigen and the heat shock protein are
CC non-covalently bound, and (c) treating an infectious disease or cancer by
CC administering a hybrid antigen and a heat shock protein. The heat shock
CC protein is preferably hsp70. The composition is administered via oral or
CC parenteral route. The hybrid antigen is useful in preparing a composition
CC for treating or preventing cancer or infectious disease. The new peptide
CC linkers give the antigens improved activity. Note: Many of the SEQ ID Nos
CC are replicated more than once in the specification but the sequences of
CC these replicated SEQ ID Nos are not the same. This sequence represents a
CC heat shock protein binding sequence.
XX
XX

SQ Sequence 8 AA;

Query Match 38.9%; Score 28; DB 8; Length 8;
Best Local Similarity 71.4%; Pred. No. 2.1e+06;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 9 VKSLYLIG 15
 |||||
 Db 1 VKRLYIG 7

RESULT 10
 ID ADU08841
 ADU08841 standard; peptide; 8 AA.

AC ADU08841;

DT 13-JAN-2005 (first entry)

DE Heat shock protein binding domain #491.

KM Hybrid antigen; antigenic domain; infectious agent; tumour antigen;

KM binding domain; heat shock protein; hsp; immune response;

KM infectious disease; cancer; cytostatic; antimicrobial; immunostimulant.

OS Unidentified.

PN WO2004091493-A2.

PD 28-OCT-2004.

PF 09-APR-2004; 2004MO-US010983.

PR 11-APR-2003; 2003US-0462469P.

PR 18-APR-2003; 2003US-0463746P.

PR 16-SEP-2003; 2003US-0503417P.

PR 12-FEB-2004; 2004US-00776521.

PR 13-FEB-2004; 2004MO-US004340.

PR 08-APR-2004; 2004US-00820067.

XX (MOJA-) MOJAVE THERAPEUTICS INC.

PI Flechtner JB, Prince-Cohane K, Mehra S, Slusaregicz P, Andjelic S;

PI Barber BH;

DR WPI; 2004-775516/76.

XX Hybrid antigen useful for treating an infectious disease or cancer,

PT comprises an antigenic domain from the infectious agent or cancer joined

PT to a heat shock protein binding domain through an improved linker

PT peptide.

XX Disclosure; Page 44; 99pp; English.

XX The invention relates to hybrid antigens comprising at least one

CC antigenic domain of an infectious agent or tumour antigen, at least one

CC binding domain that non-covalently binds to a heat shock protein (hsp),

CC and at least one peptide linker between them. Also disclosed are: (a) a

CC composition for inducing an immune response to an infectious agent or

CC tumour antigen comprising at least one of the hybrid antigens or a

CC complex of at least one heat shock protein and at least one of the hybrid

CC antigen, (b) a method for inducing an immune response to an infectious

CC agent or tumour antigen by administering a hybrid antigen and a heat

CC shock protein, where the hybrid antigen and the heat shock protein are

CC non-covalently bound, and (c) treating an infectious disease or cancer by

CC administering a hybrid antigen and a heat shock protein. The heat shock

CC protein is preferably hsp70. The composition is administered via oral or

CC parenteral route. The hybrid antigen is useful in preparing a composition

CC for treating or preventing cancer or infectious disease. The new peptide

CC linkers give the antigens improved activity. Note: Many of the SEQ ID Nos

CC are replicated more than once in the specification but the sequences of

CC these replicated SEQ ID Nos are not the same. This sequence represents a

CC heat shock protein binding sequence.

XX Sequence 8 AA;

XX Query Match 38.9%; Score 28; DB 8; Length 8;

Best Local Similarity 71.4%; Pred. No. 2.1e+06;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 VKSLYLIG 15
 |||||
 Db 1 VKRLYIG 7

RESULT 11
 ID ADT73328
 ADT73328 standard; peptide; 9 AA.

AC ADT73328;

DT 13-JAN-2005 (first entry)

DE Human RSV N high affinity binding peptide SegID 1224.

XX human respiratory syncytial virus; cytotoxic T lymphocyte; CTL;

KM MHC epitope; DNA-based immunisation; RSV infection; virucidal; vaccine.

XX Human respiratory syncytial virus.

XX WO2004092207-A2.

PD 28-OCT-2004.

PF 16-APR-2004; 2004MO-EP004061.

PR 16-APR-2003; 2003EP-00447095.

PR (ALGO-) ALGONOMICS NV.

PI Lasters I, Desmet J, Stegmann T;

PI WPI; 2004-758334/74.

DR New respiratory syncytial virus (RSV) peptides (e.g. G, M, M2-1, M2-2, N

PT or P) for inducing an immune response to RSV or for diagnosing,

PT preventing or treating viral infections, particularly RSV infection.

XX Disclosure; SEQ ID NO 1224; 143pp; English.

XX This invention relates to novel isolated or purified peptides of the

CC human respiratory syncytial virus (RSV), in particular ten RSV genes

CC encoding 11 separate viral proteins: non-structural proteins NS-1 (also

CC known as the 1C protein) & NS-2 (1B protein), a polymerase protein L and

CC eight structural proteins preferably G, also M, M2-1, M2-2, N, P, F, and

CC SH (also known as the 1A protein). Specifically, it refers to a

CC composition comprising an above peptide mixed with a pharmaceutical

CC excipient or an RSV immunogenic composition comprising a recombinant

CC expression vector with a nucleic acid insert encoding an above peptide.

CC The present invention describes an in vitro method of detecting cytotoxic

CC T lymphocytes (CTLs) that respond to a major histocompatibility complex

CC (MHC) class I restricted T-cell stimulating peptide epitope of RSV. The

CC RSV peptide is useful for preparing a diagnostic composition or an RSV

CC (prophylactic or therapeutic) vaccine composition for a DNA-based

CC immunisation, or for preparing an immune response provoking vaccine in

CC the event of RSV infection (the vaccine being prepared by contacting the

CC polypeptide in an immune response-provoking amount of specific CTL).

CC Accordingly, these peptide compositions have virucidal activity. This

CC peptide sequence is a human RSV high binding affinity peptide of the

CC invention.

XX Sequence 9 AA;

XX Query Match 38.9%; Score 28; DB 8; Length 9;

XX Best Local Similarity 66.7%; Pred. No. 2.1e+06;

XX Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

XX QY 6 AKSVKSLYL 14
 |||||
 Db 1 AKSVKNIML 9

```
RESULT 12
AAE00650
ID AAE00650 standard; protein; 11 AA.
XX
XX AAE00650;
AC
XX
XX 02-JUL-2001 (first entry)
XX
XX Alpha-1,2 mannosidase protein #2.
XX
XX Alpha-1,2 mannosidase; glycosylation pattern; glycoprotein.
XX
XX Unidentified.
OS
XX
XX Key Location/Qualifiers
FH Misc-difference 2
FT /label= Unknown
FT
XX
XX WO200125406-A1.
XX
XX 12-APR-2001.
XX
XX 02-OCT-2000; 2000WO-US027210.
XX
XX 01-OCT-1999; 99US-0157341P.
XX
XX (UUYI-) UNIV VICTORIA INNOVATION & DEV CORP.
XX
XX Hintz WE, Eades CJ;
XX
XX WPI; 2001-290610/30.
XX
XX New mannosidase enzymes, useful for modifying or altering the
PT glycosylation patterns of macromolecules, particularly for modifying
PT target protein.
XX
XX Example 9; Page 40; 87pp; English.
XX
XX The invention relates to Aspergillus nidulans alpha-1,2 mannosidase genes
CC and proteins. The mannosidase enzymes are useful for modifying or
CC altering the glycosylation patterns of macromolecules, e.g. protein. In
CC particular, the enzymes useful for modifying target proteins. This
CC enables glycoproteins to be engineered to be more effectively used and
CC produced. The present sequence is alpha-1,2 mannosidase protein. The
CC MARRENV3B forward primer is designed from the complement of the reverse
CC translation of this sequence. Note: This sequence is stated as being the
CC same as that shown as SEQ ID NO:14 in the sequence listing of the
CC specification. However this sequence has additional 2 residues at its N-
CC terminal end
XX
XX Sequence 11 AA;
SQ
Query Match 38.9%; Score 28; DB 4; Length 11;
Best Local Similarity 45.5%; Pred. No. 4.7e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

```
XX
XX Virus; adenovirus; poxvirus; alphavirus; immune response; gp100;
XX tumour antigen; CEA; carcinoembryonic antigen; immunostimulant;
XX cytostatic; immunotherapy; interferon-gamma; IFN-gamma; cancer.
XX
XX Viruses.
OS
XX Synthetic.
XX
XX WO200130382-A1.
XX
XX 03-MAY-2001.
XX
XX 20-OCT-2000; 2000WO-CA001253.
XX
XX 22-OCT-1999; 99US-0160879P.
XX
XX 07-AUG-2000; 2000US-0223325P.
XX
XX (AVET ) AVENTIS PASTEUR LTD.
XX
XX Bernstein N, Tartaglia J, Moingeon P, Barber B;
XX
XX WPI; 2001-308587/32.
XX
XX Inducing immune response to tumor antigen, useful in immunotherapy of
PT cancer, by administering the antigen to a lymphatic site.
XX
XX Example 1; Page 39; 60pp; English.
XX
XX The present invention describes a method for inducing an immune response,
CC in an animal, to a tumour antigen (Ag) comprising administering Ag, or
CC nucleic acid (I) that encodes it, to a lymphatic site. Cynomolgus monkeys
CC (Macaca fascicularis) were injected with a modified form of gp100 antigen
CC (a) into the left inguinal lymph node or (b) subcutaneously. Both animals
CC of (a) developed a cell-mediated response (indicated by production of
CC interferon-gamma from T lymphocytes when exposed to gp100 peptides), but
CC only 2 of 4 animals of (b) did so. Also animals in (a) produced a far
CC greater antibody response to gp100. The method is used in immunotherapy
CC of a wide range of cancers through induction of a specific immune
CC response (humoral and cellular) against the tumour antigens. When
CC administered to a lymphatic site, Ag (or (I)) induces a stronger immune
CC response than administration by other routes and may also break tolerance
CC to Ag. AAB97708 and AAB97709 represent gp100 epitopes; AAB97710 to
CC AAB97815 represent peptides derived from gp100 which stimulate interferon
CC (IFN)-gamma production; AAH20120 encodes the modified gp100 protein given
CC in AAB97816; AAH20121 encodes the modified carcinoembryonic antigen (CEA)
CC protein given in AAB97817; and AAB97818 represents a CEA modified antigen
CC peptide, all of which are used in the exemplification of the present
CC invention. (Updated on 06-AUG-2003 to correct OS field.)
XX
XX Sequence 15 AA;
SQ
Query Match 38.9%; Score 28; DB 4; Length 15;
Best Local Similarity 75.0%; Pred. No. 6.7e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

KM cytostatic; immunotherapy; interferon-gamma; IFN-gamma; cancer.
 XX
 OS Varuses.
 OS Synthetic.
 XX
 PN WO200130382-A1.
 XX
 PD 03-MAY-2001.
 XX
 PF 20-OCT-2000; 2000WO-CA001253.
 XX
 PR 22-OCT-1999; 99US-0160879P.
 PR 07-AUG-2000; 2000US-0223325P.
 XX
 PA (AVET) AVENTIS PASTEUR LTD.
 XX
 PI Berinstein N, Tartaglia J, Moingeon P, Barber B;
 DR WPI; 2001-308587/32.
 XX
 PT Inducing immune response to tumor antigen, useful in immunotherapy of
 cancer, by administering the antigen to a lymphatic site.
 XX
 PS Example 1; Page 39; 60pp; English.
 XX
 CC The present invention describes a method for inducing an immune response,
 CC in an animal, to a tumour antigen (Ag) comprising administering Ag, or
 CC nucleic acid (I) that encodes it, to a lymphatic site. Cynomolgus monkeys
 CC (Macaca fascicularis) were injected with a modified form of gp100 antigen
 CC (a) into the left inguinal lymph node or (b) subcutaneously. Both animals
 CC of (a) developed a cell-mediated response (indicated by production of
 CC interferon-gamma from T lymphocytes when exposed to gp100 peptides), but
 CC only 2 of 4 animals of (b) did so. Also animals in (a) produced a far
 CC greater antibody response to gp100. The method is used in immunotherapy
 CC of a wide range of cancers through induction of a specific immune
 CC response (humoral and cellular) against the tumour antigens. When
 CC administered to a lymphatic site, Ag (or (I)) induces a stronger immune
 CC response than administration by other routes and may also break tolerance
 CC to Ag. AAB97708 and AAB97709 represent gp100 epitopes; AAB97710 to
 CC AAB97815 represent peptides derived from gp100 which stimulate interferon
 CC (IFN)-gamma production; AAH20120 encodes the modified gp100 protein given
 CC in AAB97816; AAH20121 encodes the modified carcinoembryonic antigen (CEA)
 CC protein given in AAB97817; and AAB97818 represents a CEA modified antigen
 CC peptide, all of which are used in the exemplification of the present
 CC invention. (Updated on 06-AUG-2003 to correct OS field.)
 CC
 SQ Sequence 15 AA:
 Query Match 38.9%; Score 28; DB 4; Length 15;
 Best Local Similarity 75.0%; Pred. No. 6,7e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 VPFSVAKS 8
 |||||:
 DB 3 VPFSVSVS 10
 RESULT 15
 AAB98135
 ID AAB98135 standard; peptide; 15 AA.
 XX
 AC AAB98135;
 XX
 DT 17-AUG-2001 (first entry)
 XX
 DE Interferon-gamma stimulation gp100 derived peptide 1369.
 XX
 KM Human; gp100; immune system; H6 promoter; Vaccinia virus; gp100M;
 KM modified gp100; vaccine; gene therapy; cancer.
 XX
 OS Homo sapiens.
 OS
 PN WO200130847-A1.

XX
 PD 03-MAY-2001.
 XX
 PF 20-OCT-2000; 2000WO-CA001254.
 XX
 PR 22-OCT-1999; 99US-0160879P.
 PR 07-AUG-2000; 2000US-0223325P.
 XX
 PA (AVET) AVENTIS PASTEUR LTD.
 XX
 PI Berinstein N, Tartaglia J, Moingeon P, Barber B, Tine JA;
 DR WPI; 2001-316326/33.
 XX
 PT New isolated and purified gp100 useful for the prophylactic treatment of
 cancer.
 XX
 PS Example 4; Page 61; 89pp; English.
 XX
 CC The present invention describes an isolated and purified modified gp100
 CC molecule (gp100M) capable of modulating an immune response in an animal.
 CC gp100M has cytostatic activity and can be used in vaccine production and
 CC gene therapy. Nucleic acids and proteins of the invention are useful as
 CC vaccines for prophylactic treatment of cancer. AAH22084 to AAH22106 and
 CC AAB98098 to AAB98206 represent sequence used in the exemplification of
 CC the present invention. More specifically AAB98098 to AAB98205 represent
 CC peptides derived from gp100; AAH22084 to AAH22097 and AAH22100 to
 CC AAH22106 represent primers used in the present invention; AAH22099
 CC represents the plasmid nucleotide sequence comprising the Vaccinia virus
 CC H6 promoter and the human gp100 gene; and AAH22098 encodes the human
 CC gp100M protein given in AAB22106
 XX
 SQ Sequence 15 AA:
 Query Match 38.9%; Score 28; DB 4; Length 15;
 Best Local Similarity 75.0%; Pred. No. 6,7e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 VPFSVAKS 8
 |||||:
 DB 3 VPFSVSVS 10
 RESULT 16
 AAB98134
 ID AAB98134 standard; peptide; 15 AA.
 XX
 AC AAB98134;
 XX
 DT 17-AUG-2001 (first entry)
 XX
 DE Interferon-gamma stimulation gp100 derived peptide 1368.
 XX
 KM Human; gp100; immune system; H6 promoter; Vaccinia virus; gp100M;
 KM modified gp100; vaccine; gene therapy; cancer.
 XX
 OS Homo sapiens.
 OS
 PN WO200130847-A1.
 XX
 PD 03-MAY-2001.
 XX
 PF 20-OCT-2000; 2000WO-CA001254.
 XX
 PR 22-OCT-1999; 99US-0160879P.
 PR 07-AUG-2000; 2000US-0223325P.
 XX
 PA (AVET) AVENTIS PASTEUR LTD.
 XX
 PI Berinstein N, Tartaglia J, Moingeon P, Barber B, Tine JA;
 DR WPI; 2001-316326/33.
 XX

PT New isolated and purified gp100 useful for the prophylactic treatment of
 PT cancer.
 XX
 PS Example 4; Page 61; 89pp; English.
 XX
 CC The present invention describes an isolated and purified modified gp100
 CC molecule (gp100M) capable of modulating an immune response in an animal.
 CC gp100M has cytostatic activity and can be used in vaccine production and
 CC gene therapy. Nucleic acids and proteins of the invention are useful as
 CC vaccines for prophylactic treatment of cancer. AAH22084 to AAH22106 and
 CC AAB98098 to AAB98206 represent sequence used in the exemplification of
 CC the present invention. More specifically AAB98098 to AAB98205 represent
 CC peptides derived from gp100; AAH22084 to AAH22097 and AAH22100 to
 CC AAH22106 represent primers used in the present invention; AAH22099
 CC represents the plasmid nucleotide sequence comprising the Vaccinia virus
 CC H6 promoter and the human gp100 gene; and AAH22098 encodes the human
 CC gp100M protein given in AAB22106
 CC
 XX
 SQ Sequence 15 AA;
 Query Match 38.9%; Score 28; DB 4; Length 15;
 Best Local Similarity 75.0%; Pred. No. 6.7e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 VPPSVAKS 8
 DB 8 VPPSVSVS 15
 RESULT 17
 ABR73086
 ID ABR73086 standard; peptide; 15 AA.
 XX
 AC ABR73086;
 XX
 DT 17-JUN-2003 (first entry)
 XX
 DE Amino acid sequence of an epitope derived from KSHV.
 XX
 KW Epitope; KSHV; CD8 T cell; vaccine; dendritic cell; T lymphocyte.
 XX
 OS Synthetic.
 OS Kaposi's sarcoma herpesvirus.
 XX
 PN WO2003014154-A2.
 XX
 XX 20-FEB-2003.
 PD
 PF 05-AUG-2002; 2002WO-GB003594.
 XX
 PR 03-AUG-2001; 2001GB-00019038.
 XX
 PA (UNLO) UNIV COLLEGE LONDON.
 XX
 PI Boshoff C;
 XX
 DR WPI; 2003-289909/28.
 XX
 PT New polypeptides and expression vectors with an epitope sequence
 PT recognized by a CD8 T cell, useful in the manufacture of a vaccine for
 PT the prophylactic and/or therapeutic treatment of Kaposi's sarcoma
 PT herpesvirus infection.
 PT
 XX
 PS Claim 2; Page 49; 58pp; English.
 XX
 CC The present sequence represents an epitope, of a formula given in the
 CC specification. The epitope is derived from Kaposi's sarcoma herpesvirus
 CC (KSHV), and is recognised by CD8 T cells. Polypeptides comprising the
 CC epitope are useful for producing a vaccine against KSHV. They are also
 CC useful for stimulating dendritic cells or T lymphocytes ex vivo
 XX
 SQ Sequence 15 AA;

Query Match 38.9%; Score 28; DB 6; Length 15;
 Best Local Similarity 62.5%; Pred. No. 6.7e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 8 SVKSLYL 15
 DB 8 SLSSLYLG 15
 RESULT 18
 ABR30675
 ID ABR30675 standard; peptide; 15 AA.
 XX
 AC ABR30675;
 XX
 DT 19-MAY-2003 (first entry)
 XX
 DE Human cancer-related protein 83P4B8 HLA peptide #1737.
 XX
 KW Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.
 XX
 OS Homo sapiens.
 XX
 PN WO200283921-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 10-APR-2002; 2002WO-US011654.
 XX
 PR 10-APR-2001; 2001US-0282739P.
 XX
 PR 10-APR-2001; 2001US-0283112P.
 XX
 PR 25-APR-2001; 2001US-0286630P.
 XX
 PA (AGEN-) AGENSYS INC.
 XX
 PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raltano AB;
 XX
 DR WPI; 2003-075555/07.
 XX
 PT New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response in
 PT cancer patients.
 XX
 PS Claim 13; Page 479; 1021pp; English.
 XX
 CC The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention
 XX
 SQ Sequence 15 AA;
 Query Match 38.9%; Score 28; DB 6; Length 15;
 Best Local Similarity 63.6%; Pred. No. 6.7e+02;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 4 SVAKSVKSLYL 14
 DB 2 SVKSFKDLQL 12

RESULT 19

ABR31599
 ID ABR31599 standard; peptide; 15 AA.
 XX
 AC ABR31599;
 XX
 DT 19-MAY-2003 (first entry)
 XX
 DE Human cancer-related protein 83P4B8 HLA peptide #2661.
 XX
 KM Human; cytostatic; vaccine; cancer; immune response; HLA;
 XX human leukocyte antigen.
 OS Homo sapiens.
 XX WO200283921-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 10-APR-2002; 2002WO-US011654.
 XX
 PR 10-APR-2001; 2001US-0282739P.
 PR 10-APR-2001; 2001US-0283112P.
 PR 25-APR-2001; 2001US-0286630P.
 XX
 PA (AGEN-) AGENSYS INC.
 XX
 PI Jakobovits A, Challita-Bid PM, Faris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 DR WPI; 2003-075555/07.
 XX
 PT New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response in
 PT cancer patients.
 XX
 PS Claim 13; Page 495; 1021pp; English.
 XX
 CC The present invention relates to novel human cancer-related genes and
 CC proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention
 CC
 SO Sequence 15 AA;
 XX
 QY Query Match 38.9%; Score 28; DB 6; Length 15;
 Best Local Similarity 63.6%; Pred. No. 6,7e+02;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 XX
 DB 4 SVAKSVKSLYL 14
 3 SVVKSFDLQL 13
 XX
 RESULT 20
 ID ABR31127 standard; peptide; 15 AA.
 XX
 AC ABR31127;
 XX
 DT 19-MAY-2003 (first entry)
 XX
 DE Human cancer-related protein 83P4B8 HLA peptide #2189.
 XX
 KM Human; cytostatic; vaccine; cancer; immune response; HLA;

KM human leukocyte antigen.
 XX
 OS Homo sapiens.
 XX
 PN WO200283921-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 10-APR-2002; 2002WO-US011654.
 XX
 PR 10-APR-2001; 2001US-0282739P.
 PR 10-APR-2001; 2001US-0283112P.
 PR 25-APR-2001; 2001US-0286630P.
 XX
 PA (AGEN-) AGENSYS INC.
 XX
 PI Jakobovits A, Challita-Bid PM, Faris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 DR WPI; 2003-075555/07.
 XX
 PT New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response in
 PT cancer patients.
 XX
 PS Claim 13; Page 487; 1021pp; English.
 XX
 CC The present invention relates to novel human cancer-related genes and
 CC proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention
 CC
 SO Sequence 15 AA;
 XX
 QY Query Match 38.9%; Score 28; DB 6; Length 15;
 Best Local Similarity 63.6%; Pred. No. 6,7e+02;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 XX
 DB 4 SVAKSVKSLYL 14
 2 SVVKSFDLQL 12
 XX
 RESULT 21
 ID ABR30768 standard; peptide; 15 AA.
 XX
 AC ABR30768;
 XX
 DT 19-MAY-2003 (first entry)
 XX
 DE Human cancer-related protein 83P4B8 HLA peptide #1830.
 XX
 KM Human; cytostatic; vaccine; cancer; immune response; HLA;
 KM human leukocyte antigen.
 OS Homo sapiens.
 XX
 PN WO200283921-A2.
 XX
 PD 24-OCT-2002.
 XX
 PR 10-APR-2002; 2002WO-US011654.
 XX

PR 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
DR WPI; 2003-075555/07.
XX
XX
PT New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX
XX
PS Claim 13; Page 481; 1021pp; English.
XX
XX The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
SQ Sequence 15 AA;
XX
XX
Query Match 38.9%; Score 28; DB 6; Length 15;
Best Local Similarity 63.6%; Pred. No. 6.7e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 4 SVAKSVKSLYL 14
DB 2 SVVKSFKDLQL 12
XX
XX
RESULT 22
ABR31373
ID ABR31373 standard; peptide; 15 AA.
XX
AC ABR31373;
XX
XX 19-MAY-2003 (first entry)
XX
XX Human cancer-related protein 83P4B8 HLA peptide #2435.
DE
XX
XX Human; cytostatic; vaccine; cancer; immune response; HLA;
KM human leukocyte antigen.
XX
XX Homo sapiens.
OS
XX WO200283921-A2.
PN
XX 24-OCT-2002.
PD
XX 10-APR-2002; 2002WO-US011654.
PF
XX 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX
XX (AGEN-) AGENSYS INC.
PA
XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
XX WPI; 2003-075555/07.
DR

XX
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX
XX
PS Claim 13; Page 491; 1021pp; English.
XX
XX The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
SQ Sequence 15 AA;
XX
XX
Query Match 38.9%; Score 28; DB 6; Length 15;
Best Local Similarity 63.6%; Pred. No. 6.7e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 4 SVAKSVKSLYL 14
DB 3 SVVKSFKDLQL 13
XX
XX
RESULT 23
ABR30871
ID ABR30871 standard; peptide; 15 AA.
XX
AC ABR30871;
XX
XX 19-MAY-2003 (first entry)
XX
XX Human cancer-related protein 83P4B8 HLA peptide #1933.
DE
XX
XX Human; cytostatic; vaccine; cancer; immune response; HLA;
KM human leukocyte antigen.
XX
XX Homo sapiens.
OS
XX WO200283921-A2.
PN
XX 24-OCT-2002.
PD
XX 10-APR-2002; 2002WO-US011654.
PF
XX 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX
XX (AGEN-) AGENSYS INC.
PA
XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
XX WPI; 2003-075555/07.
DR
XX
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX
XX
PS Claim 13; Page 482; 1021pp; English.
XX
XX The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and

CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention

XX SQ Sequence 15 AA;

Query Match 38.9%; Score 28; DB 6; Length 15;
 Best Local Similarity 63.6%; Pred. No. 6.7e+02;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 SVAKSVKSLYL 14
 Db 3 SVVKSFKDLQL 13

RESULT 24

ID ADN71829 standard; peptide; 15 AA.

XX ADN71829;

DT 01-JUL-2004 (first entry)

DE Human 273P4B7v.1 protein epitope #5792.

XX 273P4B7; human; cancer; tumour; epitope.

OS Homo sapiens.

PN WO2004016762-A2.

PD 26-FEB-2004.

PF 15-AUG-2003; 2003WO-US025665.

PR 16-AUG-2002; 2002US-0404306P.

PR 01-NOV-2002; 2002US-0423290P.

XX (AGEN-) AGENSYS INC.

PI Chailita-Eid PM, Faris M, Raitano AB, Jakobovits A, Ge W;

DR WPI; 2004-203790/19.

PT New composition comprising 273P4B7 proteins, useful for detecting and
 treating cancer by inhibiting the growth or viability of cancer cells.

XX Claim 1; Fig 2A; 268bp; English.

CC The invention relates to a composition comprising 273P4B7 proteins. The
 CC composition and proteins are useful for detecting and treating cancer by
 CC inhibiting the growth or viability of cancer cells. The present sequence
 CC represents the amino acid sequence of a human 273P4B7v.1 protein epitope.
 CC Note the epitope sequences are displayed in tables VIII-XLIX.

XX SQ Sequence 15 AA;

Query Match 38.9%; Score 28; DB 8; Length 15;
 Best Local Similarity 54.5%; Pred. No. 6.7e+02;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 VPFSVAKSVKS 11
 Db 3 IPSSVKNKSMNS 13

RESULT 25

ID ADN71169 standard; peptide; 15 AA.

XX ADN71169;

DT 01-JUL-2004 (first entry)

DE Human 273P4B7v.1 protein epitope #5132.

XX 273P4B7; human; cancer; tumour; epitope.

OS Homo sapiens.

PN WO2004016762-A2.

PD 26-FEB-2004.

PF 15-AUG-2003; 2003WO-US025665.

PR 16-AUG-2002; 2002US-0404306P.

PR 01-NOV-2002; 2002US-0423290P.

XX (AGEN-) AGENSYS INC.

PI Chailita-Eid PM, Faris M, Raitano AB, Jakobovits A, Ge W;

DR WPI; 2004-203790/19.

PT New composition comprising 273P4B7 proteins, useful for detecting and
 treating cancer by inhibiting the growth or viability of cancer cells.

XX Claim 1; Fig 2A; 268bp; English.

CC The invention relates to a composition comprising 273P4B7 proteins. The
 CC composition and proteins are useful for detecting and treating cancer by
 CC inhibiting the growth or viability of cancer cells. The present sequence
 CC represents the amino acid sequence of a human 273P4B7v.1 protein epitope.
 CC Note the epitope sequences are displayed in tables VIII-XLIX.

XX SQ Sequence 15 AA;

Query Match 38.9%; Score 28; DB 8; Length 15;
 Best Local Similarity 54.5%; Pred. No. 6.7e+02;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 VPFSVAKSVKS 11
 Db 4 IPSSVKNKSMNS 14

RESULT 26

ID ADN71392 standard; peptide; 15 AA.

XX ADN71392;

DT 01-JUL-2004 (first entry)

DE Human 273P4B7v.1 protein epitope #5355.

XX 273P4B7; human; cancer; tumour; epitope.

OS Homo sapiens.

PN WO2004016762-A2.

PD 26-FEB-2004.

PF 15-AUG-2003; 2003WO-US025665.

PR 16-AUG-2002; 2002US-0404306P.

PR 01-NOV-2002; 2002US-0423290P.

CC sequence of the major allergens of cereal pollen. The invention also
CC describes; 1) DNA that hybridizes to the novel cereal allergens under
CC stringent conditions and is derived from Poaceae; 2) DNA that encodes a
CC polypeptide that is immunologically cross-reactive with the major
CC allergens Sec c 4 from Secale cereale, Hor v 4 from Hordeum vulgare or
CC Tri a 4 from Triticum aestivum and derived from Poaceae; 3) a DNA
CC fragment, or combination of fragments, that encode an immunomodulatory T-
CC cell reactive fragment of Group 4 Poaceae allergens; 4) a DNA
CC corresponding to any of the new DNAs or fragments that encodes an
CC immunomodulatory T-cell reactive fragment but is modified by targeted
CC mutation of individual codons, deletion or addition; 5) a recombinant DNA
CC expression vector or cloning system containing any of the new DNAs linked
CC to expression control sequences; 6) a host organism transformed with any
CC of the new DNAs or the vector of 5) and 7) preparing a polypeptide
CC encoded by the new DNAs by culturing the organisms of 6). Primers were
CC designed from the known DNA sequence for the Phl p 4 (Phleum pratense)
CC allergen and tested for amplification of DNA from rye pollen. The partial
CC sequences obtained were used to screen expressed sequence tag (EST) data
CC bases; the partial sequences aligned and new primers designed for
CC amplification of further sequence fragments, allowing construction of the
CC sequences (two isoforms) for Sec c 4. The Sec c 4 sequences obtained were
CC used to screen EST data bases from wheat and barley to identify the other
CC novel polypeptides. The novel polynucleotides and vectors containing
CC them, are used for immunotherapeutic vaccination against allergies
CC induced by Group 4 Poaceae allergens. Polypeptides can be used similarly,
CC also for diagnosis (in vivo or in vitro) of such allergies or in a
CC vaccine. This sequence represents a group 4 allergenic peptide from
CC Cynodon dactylon (bermuda grass).

CC Sequence 11 AA;

Query Match 37.5%; Score 27; DB 9; Length 11;
Best Local Similarity 62.5%; Pred. No. 7.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 7 KSVKSLYL 14
||:|:|:|:
Db 1 KTVKPLYL 8

RESULT 32
AEB13465
ID AEB13465 standard; peptide; 11 AA.

AC AEB13465;

DT 08-SEP-2005 (first entry)

DE Cynodon dactylon group 4 allergen fragment SEQ ID NO 11.

KW grass pollen; allergen; Lol p 4; pollen; diagnosis; vaccine;
KM group 4 allergen.

OS Cynodon dactylon.

PN WO2005058936-A2.

PD 30-JUN-2005.

PF 01-DEC-2004; 2004WO-EP013663.

PR 16-DEC-2003; 2003DE-01059352.

PA (MERE) MERCK PATENT GMBH.

PI Fiebig H, Nandy A, Cromwell O;

DR WPI; 2005-506110/51.

For the treatment/prevention of the main grass pollen allergies, a DNA
PT molecule is selected for hybridizing to give a wide variety of agents
PT with a hypoallergenic effect.

PS Disclosure; SEQ ID NO 11; 38pp; German.

XX This invention describes a novel method for the preparation of a DNA
CC molecule encoding the main grass pollen allergen Lol p 4. The invention
CC also describes fragments, new combinations of partial sequences and point
CC mutants which have a hypoallergenic effect. The recombinant DNA molecules
CC and the derived polypeptides, fragments, combinations of partial
CC sequences and variants are for the treatment of pollen allergies. They
CC can also be used for in vitro and in vivo diagnosis of pollen allergies.
CC The products of the invention can be used as a pharmaceutical for
CC immunotherapeutic vaccination against Lol p 4 allergies and/or for the
CC prevention of such allergies. This sequence represents a fragment of the
CC Cynodon dactylon group 4 allergen.

XX Sequence 11 AA;

Query Match 37.5%; Score 27; DB 9; Length 11;
Best Local Similarity 62.5%; Pred. No. 7.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 7 KSVKSLYL 14
||:|:|:|:
Db 1 KTVKPLYL 8

RESULT 33
ADM47132
ID ADM47132 standard; peptide; 12 AA.

AC ADM47132;

DT 24-MAR-2005 (first entry)

DE Anti-CD20 monoclonal antibody light chain MHB20-8.10 CDR 1.

KW CD20; monoclonal antibody; rheumatoid arthritis; antiarthritis;

KM antirheumatic; immune disorder; inflammation; musculoskeletal disease;

KW idiopathic thrombocytopenic purpura; hemostatic; hemolytic anemia.

OS Mus musculus.

PN WO2005000901-A2.

PD 06-JAN-2005.

PF 07-MAY-2004; 2004WO-US014326.

PR 09-MAY-2003; 2003US-0469451P.

PA (UYDU-) UNIV DUKE.

PI Tedder TF, Uchida J, Hamaguchi Y, Poe JC;

DR WPI; 2005-066556/07.

Novel monoclonal antibody (mab) binding to CD20 or mouse CD20, in which
PT density of binding of mab to B cells is two-fold higher than density of
PT binding of mab1F5 to B cells, useful for depleting B cells, and treating
PT B cell disorder.

PS Example 1; SEQ ID NO 91; 205pp; English.

XX The invention relates to a monoclonal antibody (mab) or its antigen-
CC binding fragment that specifically binds to human CD20 or mouse CD20,
CC where the density of binding of mab or antigen-binding fragment of mab 1F5
CC cells is at least two-fold higher than the density of binding of mab 1F5
CC to B cells. Also included are a pharmaceutical composition comprising mab
CC in a carrier, a pharmaceutical composition (comprising mab or its antigen
CC binding fragment which specifically binds to the same antigenic
CC determinant as a monoclonal antibody chosen from HB20-1, HB20-3, HB20-4
CC mab, and HB20-25 in a carrier), a cell line producing the mab, producing the
CC mab, an antigen binding fragment of the mab, an isolated nucleic acid
CC encoding a heavy chain or light chain comprising a variable region

CC (comprising CDR3, or CDR1, CDR2 and CDR3 regions from mab chosen from
CC HB20-1, HB20-3, HB20-4, HB20-5, HB20-25, MB20-11, MB20-2, MB20-7,
CC MB20-8, MB20-10, MB20-11, MB20-14, MB20-16 and MB20-18) a vector
CC comprising the nucleic acid, a cell comprising the nucleic acid or
CC vector, and depleting B cells in a mammalian subject (involving
CC administering the mab and anti-CD22 or anti-CD19 antibody). The anti-CD20
CC mab, compositions and cells are useful for depleting B cells in a
CC mammalian subject and for treating a B cell disorder. The B cell disorder
CC is B cell malignancy or autoimmune disease e.g. rheumatoid arthritis,
CC idiopathic thrombocytopenic purpura or hemolytic anemia. The mammalian
CC subject is resistant to anti-CD20 mab therapy or resistant to therapy
CC with mab C288. The mammalian subject has been or is currently treated
CC with chemotherapy. The mammalian subject has a relapse in a B cell
CC disorder. The mammalian subject is immunocompromised. The present
CC sequence represents a CDR (complementarity determining region) from anti-
CC CD20 monoclonal antibody.

SQ Sequence 12 AA;

Query Match 37.5%; Score 27; DB 9; Length 12;
Best Local Similarity 45.5%; Pred. No. 8e+02; Mismatches 0; Gaps 0;
Matches 5; Conservative 4; Indels 2;

QY 4 SVAKSVKSLYL 14
||: ||: ||:
1 SVSNIRSNYL 11

Db

RESULT 34
AAG64140
ID AAG64140 standard; peptide; 15 AA.

AC AAG64140;

XX 25-SEP-2001 (first entry)

DE Ribosomal protein S17 10 N-terminal peptide.

XX Ribosomal protein S17 10; cancer; haemopathy; infection;
KW human immunodeficiency virus; HIV; immunological disease;
KW inflammatory disease; cytostatic; anti-HIV; anti-inflammatory;
KW immunomodulator.

XX Unidentified.

OS

PN WO200146411-A1.

PD 28-JUN-2001.

PF 11-DEC-2000; 2000MO-CN000551.

PR 21-DEC-1999; 99CN-00125667.

XX (UYFU-) UNIV FUDAN.

PA (SHAN-) SHANGHAI BIO DOOR GENE TECHNOLOGY LTD.

PI Mao Y, Xie Y;

PI WPI; 2001-441673/47.

DR Ribosomal protein S17 10 and encoded polynucleotide, applicable in
PT diagnosis and treatment of malignant tumor, hemopathy, HIV infection,
PT immunological diseases and various inflammation.

XX Example 6; Page 18; 34pp; Chinese.

XX The invention relates to an isolated polypeptide of ribosomal protein S17
CC 10 comprising a fully defined 88 amino acid sequence given in the
CC specification, or its fragment, analogue or derivative. The polypeptide
CC and the polynucleotide encoding it are useful in the diagnosis and
CC treatment of malignant tumours, haemopathy, HIV infection, immunological
CC diseases and inflammatory diseases. The polypeptide is also useful for
CC screening mimics, agonists, antagonists or inhibitors, or for peptide

CC fingerprinting identification. The polynucleotide can be used to design
CC primers for nucleic acid amplification or to design probes for
CC hybridisation reactions, or in producing gene chips or microarrays. The
CC present sequence is the N-terminus of the polypeptide of the invention
XX

SQ Sequence 15 AA;

Query Match 37.5%; Score 27; DB 4; Length 15;
Best Local Similarity 45.5%; Pred. No. 1e+03; Mismatches 0; Gaps 0;
Matches 5; Conservative 3; Indels 3;

QY 4 SVAKSVKSLYL 14
||: ||: ||:
5 TVVKSIRFYTL 15

Db

RESULT 35
ADG73517
ID ADG73517 standard; peptide; 15 AA.

AC ADG73517;

XX 11-MAR-2004 (first entry)

DE E faecalis methionine aminopeptidase type I (MAP) tryptic peptide 3.

XX (5-methylaminomethyl-2-thiouridylate)-methyltransferase; antibacterial;
KW bacterial infection; antimicrobial; disinfectant; soap; additive;
KW culture media; enzyme; tryptic digestion;
KW methionine aminopeptidase type I; MAP; map.

XX Enterococcus faecalis.

OS

XX WO2003083099-A2.

PN 09-OCT-2003.

PD

XX 02-APR-2003; 2003MO-CA000462.

PF 02-APR-2002; 2002US-0369511P.
PR 31-MAY-2002; 2002US-0385089P.
PR 04-JUN-2002; 2002US-0385751P.
PR 05-JUN-2002; 2002US-0386367P.
PR 05-JUN-2002; 2002US-0386553P.
PR 05-JUN-2002; 2002US-0386566P.
PR 05-JUN-2002; 2002US-0386577P.
PR 06-JUN-2002; 2002US-0386390P.
PR 06-JUN-2002; 2002US-0386601P.
PR 31-JUL-2002; 2002US-0399722P.
PR 05-NOV-2002; 2002US-0424053P.
PR 27-DEC-2002; 2002US-0436804P.
PR 27-DEC-2002; 2002US-0436834P.
PR 27-DEC-2002; 2002US-0436861P.
PR 31-DEC-2002; 2002US-0437281P.
PR 31-DEC-2002; 2002US-0437527P.

XX (AFFI-) AFFINIUM PHARM INC.

XX Edwards A, Dharamsi A, Vedadi M, Arrowsmith C, Awrey D;
PI Beattie B, Richards D, Domagala M, Houston S;
PI Mansoury K, Li Q, Nethery K, Virag C, Ng I, Ouyang H, Tai M;
PI Thalakkada R, Kanagarajah D;

XX WPI; 2003-812543/76.

DR New isolated recombinant bacterial peptides, useful as targets for
PT antibacterial agents, also screening methods and host cells that express
PT them.

XX Disclosure; Fig 99; 369pp; English.

XX The invention relates to a novel isolated recombinant polypeptide that
CC has at least one of the biological activities of (5-methylaminomethyl-2-

CC thioninyltransferase of Staphylococcus aureus. The
CC polypeptide of the invention demonstrates antibacterial activity and may
CC be useful for rational design of agents that may be utilized for treating
CC bacterial infections or as general antimicrobials, for example, as
CC disinfectants, soaps or additives for culture media. The current sequence
CC is that of the (5-methylaminomethyl-2-thioninyltransferase-
CC related tryptic peptide of the invention.
XX
SQ Sequence 15 AA;
Query Match 37.5%; Score 27; DB 7; Length 15;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 10 KSLYLIG 15
|:|:|:|
Db 1 KALYLG 6
RESULT 36
ADV22635
ID ADV22635 standard; peptide; 15 AA.
XX
AC ADV22635;
XX
DT 10-MAR-2005 (first entry)
XX
DE HIV-1 Rev protein, immunogenic peptide #14.
XX
XX Vaccine; virucide; antigen; autoimmune disease; infection;
KW immune modulation; cancer; neoplasm; cytostatic; melanoma; lung tumor;
KW breast tumor; uterine cervix tumor; prostatic cancer; colon tumor;
KW pancreas tumor; stomach tumor; bladder tumor; kidney tumor;
KW Hodgkin's lymphoma.
XX
OS Human immunodeficiency virus 1.
XX
PN WO2004108753-A1.
XX
PD 16-DEC-2004.
XX
PF 10-JUN-2004; 2004WO-AU000775.
XX
PR 10-JUN-2003; 2003AU-00902875.
PR 25-MAR-2004; 2004AU-00901589.
XX
XX (UYME) UNIV MELBOURNE.
XX
PA
XX
PI Kent SJ;
XX
DR WPI; 2005-031657/03.
XX
PT Use of at least one set of peptides in the preparation of a medicament
PT for modulating an immune response, and for treating cancer or yeast,
PT viral, bacterial, protozoal and mycoplasma infections.
XX
XX
PS Disclosure; SEQ ID NO 1055; 645bp; English.
XX
XX The invention relates to the use of at least one set of peptides in the
CC preparation of a medicament for modulating an immune response, where
CC individual peptides of a respective set comprise different portions of an
CC amino acid sequence corresponding to a single polypeptide of interest and
CC display partial sequence identity or similarity to at least one other
CC peptide of the same set of peptides (i.e. they are overlapping). Also
CC included are an antigen-presenting cell which has been contacted with the
CC peptides above and thus presents the peptides, a population of such
CC antigen-presenting cells, a process for producing antigen-presenting
CC cells for modulating an immune response to a polypeptide of interest, a
CC method for producing antigen-specific lymphocytes, a composition
CC comprising at least one set of the peptides (and a carrier and/or
CC diluent), a method for modulating an immune response to a polypeptide of
CC interest comprising administering to a patient in need at least one set
CC of the peptides, a method for treatment and/or prophylaxis of a disease

CC or condition associated with the presence of a polypeptide of interest
CC and a composition of matter for modulating an immune response in a
CC subject to a target antigen. The polypeptide of interest is also a
CC disease- or condition-associated polypeptide that is a polypeptide
CC produced by a pathogenic organism or a cancer, and produced by a
CC pathogenic organism selected from yeast, viruses, bacteria, helminths,
CC protozoans and mycoplasmas. The disease- or condition-associated
CC polypeptide is produced by a cancer selected from melanoma, lung cancer,
CC breast cancer, cervical cancer, prostate cancer, colon cancer, pancreatic
CC cancer, stomach cancer, bladder cancer, kidney cancer, post transplant
CC lymphoproliferative disease (PTLD) or Hodgkin's lymphoma. The uncultured
CC antigen-presenting cells or their precursors are useful in the
CC preparation of a medicament for the treatment of a disease or condition
CC in a subject, which disease or condition is associated with the presence
CC or aberrant expression of a target antigen, where the antigen-presenting
CC cells or their precursors have not been subjected to activating
CC conditions but have been contacted with an antigen that corresponds to
CC the target antigen to express a processed or modified form of the antigen
CC for presentation to the subject's immune system. The present sequence is
CC one of a set of overlapping immunogenic peptides derived from an HIV-1
CC protein.
XX
SQ Sequence 15 AA;
Query Match 37.5%; Score 27; DB 9; Length 15;
Best Local Similarity 41.7%; Pred. No. 1e+03;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 4 SVAKSVKSLYLIG 15
|:|:|:|:|
Db 2 SISEWILSTYLIG 13
RESULT 37
AEC11117
ID AEC11117 standard; peptide; 15 AA.
XX
AC AEC11117;
XX
DT 20-OCT-2005 (first entry)
XX
DE Enterococcus faecalis methionine aminopeptidase type I peptide.
XX
KW protein purification; antibacterial; antimicrobial; infection;
KW drug screening; methionine aminopeptidase type I.
XX
XX Enterococcus faecalis.
XX
OS
XX
PN US2005181388-A1.
XX
PD 18-AUG-2005.
XX
PF 04-OCT-2004; 2004US-00958216.
XX
PR 02-APR-2002; 2002US-0369511P.
PR 04-APR-2002; 2002US-0369817P.
PR 04-APR-2002; 2002US-0370102P.
PR 08-APR-2002; 2002US-0370778P.
PR 08-APR-2002; 2002US-0370929P.
PR 08-APR-2002; 2002US-0370820P.
PR 08-APR-2002; 2002US-0370859P.
PR 08-APR-2002; 2002US-0370899P.
PR 08-APR-2002; 2002US-0370915P.
PR 09-APR-2002; 2002US-0371067P.
PR 09-APR-2002; 2002US-0371107P.
PR 09-APR-2002; 2002US-0371140P.
PR 09-APR-2002; 2002US-0371185P.
PR 31-MAY-2002; 2002US-0385089P.
PR 31-MAY-2002; 2002US-0385426P.
PR 04-JUN-2002; 2002US-0385751P.
PR 05-JUN-2002; 2002US-0386018P.
PR 05-JUN-2002; 2002US-0386367P.
PR 05-JUN-2002; 2002US-0386548P.

PR 05-JUN-2002; 2002US-0386553P.
 PR 05-JUN-2002; 2002US-0386566P.
 PR 05-JUN-2002; 2002US-0386577P.
 PR 06-JUN-2002; 2002US-0386283P.
 PR 06-JUN-2002; 2002US-0386399P.
 PR 06-JUN-2002; 2002US-0386430P.
 PR 06-JUN-2002; 2002US-0386601P.
 PR 06-JUN-2002; 2002US-0386826P.
 PR 06-JUN-2002; 2002US-0386869P.
 PR 31-JUL-2002; 2002US-039972P.
 PR 01-AUG-2002; 2002US-0400348P.
 PR 05-NOV-2002; 2002US-0424053P.
 PR 06-NOV-2002; 2002US-0424380P.
 PR 08-NOV-2002; 2002US-0425086P.
 PR 08-NOV-2002; 2002US-0425200P.
 PR 24-DEC-2002; 2002US-0436243P.
 PR 24-DEC-2002; 2002US-0436288P.
 PR 24-DEC-2002; 2002US-0436349P.
 PR 26-DEC-2002; 2002US-0436567P.
 PR 26-DEC-2002; 2002US-0436572P.
 PR 26-DEC-2002; 2002US-0436588P.
 PR 27-DEC-2002; 2002US-0436675P.
 PR 27-DEC-2002; 2002US-0436708P.
 PR 27-DEC-2002; 2002US-0436734P.
 PR 27-DEC-2002; 2002US-0436804P.
 PR 27-DEC-2002; 2002US-0436842P.
 PR 27-DEC-2002; 2002US-0436861P.
 PR 27-DEC-2002; 2002US-0436889P.
 PR 27-DEC-2002; 2002US-0436933P.
 PR 27-DEC-2002; 2002US-0436900P.
 PR 30-DEC-2002; 2002US-0436947P.
 PR 30-DEC-2002; 2002US-0436971P.
 PR 30-DEC-2002; 2002US-0436987P.
 PR 30-DEC-2002; 2002US-0437013P.
 PR 30-DEC-2002; 2002US-0437038P.
 PR 31-DEC-2002; 2002US-0437281P.
 PR 31-DEC-2002; 2002US-0437527P.
 PR 31-DEC-2002; 2002US-0437620P.
 PR 31-DEC-2002; 2002US-0437638P.
 PR 02-APR-2003; 2003WO-CA000462.
 PR 04-APR-2003; 2003WO-CA000464.
 PR 08-APR-2003; 2003WO-CA000481.
 PR 08-APR-2003; 2003WO-CA000485.
 XX
 XX (AFFI-) AFFINIUM PHARM INC.
 XX
 PI Edwards A, Dharamaji A, Vedadi M, Alam MZ, Arrowsmith C, Awrey DE;
 PI Beattie B, Buzadzija K, Canadien V, Domagala M, Houston S;
 PI Kanagarajah D, Li Q, Mansoury K, McDonald M, Nethery-Brook K, Ng I;
 PI Ouyang H, Pinder B, Richards D, Tai M, Thalakada R, Vallee F;
 PI Virag C;
 XX
 XX WPI; 2005-628189/64.
 XX
 PT New composition comprising purified polypeptides from bacteria (e.g.
 PT Escherichia coli), useful for diagnosing, preventing or treating
 PT microbial infections, or in pharmacogenomic or drug screening procedures.
 XX
 PS Example 1; Fig 99; 667pp; English.
 XX
 CC The invention relates to a composition (I) comprising purified
 CC polypeptides from bacteria. Also described: (1) a crystallized,
 CC recombinant polypeptide comprising an amino acid sequence of (I), where
 CC the polypeptide is in crystal form; (2) a crystallized complex comprising
 CC the crystallized, recombinant polypeptide and a co-factor or a small
 CC organic molecule, where the complex is in crystal form; and (3) a host
 CC cell comprising a nucleic acid encoding a polypeptide of (I), where a
 CC culture of the host cell produces at least about 1 mg of the polypeptide

CC per liter of culture and the polypeptide is at least about one-third
 CC soluble as measured by gel electrophoresis. The composition and methods
 CC are useful for diagnosing, preventing or treating diseases, such as
 CC microbial infections. These may also be used in pharmacogenomic or drug
 CC screening procedures. The present sequence represents a *Enterococcus*
 CC faecalis methionine aminopeptidase type I peptide, which is used in an
 CC example from the present invention.
 XX
 SQ Sequence 15 AA;
 CC
 CC Query Match 37.5%; Score 27; DB 9; Length 15;
 CC Best Local Similarity 83.3%; Pred. No. 1e+03;
 CC Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC 10 KSLYLG 15
 CC |::|||
 CC Db 1 KALYLG 6
 CC
 CC RESULT 38
 CC ID ADT73298 standard; peptide; 9 AA.
 CC XX
 CC AC ADT73298;
 CC XX
 CC DT 13-JAN-2005 (first entry)
 CC XX
 CC DE Human RSV N high affinity binding peptide SegId 1194.
 CC XX
 CC KW human respiratory syncytial virus; cytotoxic T lymphocyte; CTL;
 CC KM MHC epitope; DNA-based immunisation; RSV infection; virucidal; vaccine.
 CC XX
 CC OS Human respiratory syncytial virus.
 CC XX
 CC FN W02004092207-A2.
 CC PN
 CC XX
 CC PD 28-OCT-2004.
 CC XX
 CC PF 16-APR-2004; 2004WO-EP004061.
 CC XX
 CC PR 16-APR-2003; 2003EP-00447095.
 CC XX
 CC PA (ALGO-) ALGONOMICS NV.
 CC XX
 CC XX Lasters I, Desmet J, Stegmann T;
 CC PI
 CC XX WPI; 2004-758334/74.
 CC DR
 CC XX
 CC PT New respiratory syncytial virus (RSV) peptides (e.g. G, M, M2-1, M2-2, N
 CC PT or P) for inducing an immune response to RSV or for diagnosing,
 CC PT preventing or treating viral infections, particularly RSV infection.
 XX
 PS Claim 11; SEQ ID NO 1194; 143pp; English.
 XX
 CC This invention relates to novel isolated or purified peptides of the
 CC human respiratory syncytial virus (RSV), in particular ten RSV genes
 CC encoding 11 separate viral proteins: non-structural proteins NS-1 (also
 CC known as the IC protein) & NS-2 (1B protein), a polymerase protein L and
 CC eight structural proteins preferably G, also M, M2-1, M2-2, N, P, F, and
 CC SH (also known as the 1A protein). Specifically, it refers to a
 CC composition comprising an above peptide mixed with a pharmaceutical
 CC excipient or an RSV immunogenic composition comprising a recombinant
 CC expression vector with a nucleic acid insert encoding an above peptide.
 CC The present invention describes an in vitro method of detecting cytotoxic
 CC T lymphocytes (CTLs) that respond to a major histocompatibility complex
 CC (MHC) class I restricted T-cell stimulating peptide epitope of RSV. The
 CC RSV peptide is useful for preparing a diagnostic composition or an RSV
 CC (prophylactic or therapeutic) vaccine composition for a DNA-based
 CC immunisation, or for preparing an immune response provoking vaccine in
 CC the event of RSV infection (the vaccine being prepared by contacting the
 CC polypeptide in an immune response-provoking amount of specific CTL).
 CC Accordingly, these peptide compositions have virucidal activity. This
 CC peptide sequence is a human RSV high binding affinity peptide of the

CC invention.
XX
SQ Sequence 9 AA;
Query Match 36.1%; Score 26; DB 8; Length 9;
Best Local Similarity 62.5%; Pred. No. 2.1e+06;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 5 VAKSVKSL 12
:|||||:
DB 2 LAKSVKNI 9
RESULT 39
ADT73299
ID ADT73299 standard; peptide; 9 AA.
XX
AC ADT73299;
XX
DT 13-JAN-2005 (first entry)
XX
DE Human RSV N high affinity binding peptide Segid 1195.
XX
KM human respiratory syncytial virus; cytotoxic T lymphocyte; CTL;
KM MHC epitope; DNA-based immunisation; RSV infection; virucidal; vaccine.
OS Human respiratory syncytial virus.
XX
PN WO2004092207-A2.
XX
XX 28-OCT-2004.
XX
PF 16-APR-2004; 2004WO-EP004061.
XX
PR 16-APR-2003; 2003EP-00447095.
XX
PA (ALGO-) ALGONOMICS NV.
XX
PI Lasters I, Desmet J, Stegmann T;
XX
DR WPI; 2004-758334/74.
XX
PT New respiratory syncytial virus (RSV) peptides (e.g. G, M, M2-1, M2-2, N
PT or P) for inducing an immune response to RSV or for diagnosing,
PT preventing or treating viral infections, particularly RSV infection.
XX
PS Claim 11; SEQ ID NO 1195; 143pp; English.
XX
CC This invention relates to novel isolated or purified peptides of the
CC human respiratory syncytial virus (RSV), in particular ten RSV genes
CC encoding 11 separate viral proteins: non-structural proteins NS-1 (also
CC known as the 1C protein) & NS-2 (1B protein), a polymerase protein L and
CC eight structural proteins preferably G, also M, M2-1, M2-2, N, P, F, and
CC SH (also known as the 1A protein). Specifically, it refers to a
CC composition comprising an above peptide mixed with a pharmaceutical
CC excipient or an RSV immunogenic composition comprising a recombinant
CC expression vector with a nucleic acid insert encoding an above peptide.
CC The present invention describes an in vitro method of detecting cytotoxic
CC T lymphocytes (CTLs) that respond to a major histocompatibility complex
CC (MHC) class I restricted T-cell stimulating peptide epitope of RSV. The
CC RSV peptide is useful for preparing a diagnostic composition or an RSV
CC (prophylactic or therapeutic) vaccine composition for a DNA-based
CC immunisation, or for preparing an immune response provoking vaccine in
CC the event of RSV infection (the vaccine being prepared by contacting the
CC polypeptide in an immune response-provoking amount of specific CTL).
CC Accordingly, these peptide compositions have virucidal activity. This
CC peptide sequence is a human RSV high binding affinity peptide of the
CC invention.
XX
SQ Sequence 9 AA;
Query Match 36.1%; Score 26; DB 8; Length 9;
Best Local Similarity 62.5%; Pred. No. 2.1e+06;

Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 5 VAKSVKSL 12
:|||||:
DB 1 LAKSVKNI 8
RESULT 40
ADK40048
ID ADK40048 standard; peptide; 10 AA.
XX
AC ADK40048;
XX
DT 06-MAY-2004 (first entry)
XX
DE PNA molecule-related transporter peptide #220.
XX
KM modified peptide nucleic acid; PNA; TP-L-PNA; TP; transporter peptide; L;
KM bond; linker; antibacterial; antimicrobial; cytostatic; virucide;
KM immunosuppressive; antisense-therapy; infectious disease;
KM bacterial infection; disinfection; cancer; bacterial; viral infection;
KM metabolic disease; immunological disorder.
XX
OS unidentified.
XX
PN WO2003092736-A2.
XX
PD 13-NOV-2003.
XX
PF 01-MAY-2003; 2003WO-DK000280.
XX
PR 01-MAY-2002; 2002DK-00000661.
XX
PA (PANT-) PANTHECO AS.
XX
PI Tolborg J, Frandsen TP, Nielsen BR, Johansen C, Kjærulff S;
XX
DR WPI; 2004-011826/01.
XX
PT New modified peptide nucleic acid (PNA) molecule, useful in treating
PT and/or preventing cancer, viral infections, metabolic diseases,
PT immunological disorders, and in particular bacterial infections.
XX
PS Claim 6; Page 84; 96pp; English.
XX
CC This invention relates to a novel modified peptide nucleic acid (PNA)
CC molecule. The invention comprises TP-L-PNA where TP transporter peptide;
CC L bond or a linker; PNA an oligomer of 4-35 monomers. The invention may
CC be useful for the development of compounds with an antibacterial,
CC antimicrobial, cytostatic, virucide or immunosuppressive. In addition,
CC the disclosed sequences could be used for antisense-therapy. The
CC compounds of the PNA molecule are useful in medicine, in particular for
CC the inactivation of the expression of specific genes by targeting the
CC genes at the mRNA, sRNA or DNA level. The PNA sequence is useful in the
CC treatment and/or prevention of infectious diseases, particularly
CC bacterial infections, or in disinfection of non-living objects. The
CC methods and compositions of the present invention are also useful for
CC treating cancer, bacterial and viral infections, metabolic diseases and
CC immunological disorders. The present sequence is that of a transporter
CC peptide which may be used during the creation of a PNA molecule of the
CC invention.
XX
SQ Sequence 10 AA;
Query Match 36.1%; Score 26; DB 8; Length 10;
Best Local Similarity 75.0%; Pred. No. 9.9e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 FSVAKSVK 10
:|||||:
DB 3 FKVAKVVK 10

RESULT 41
ABJ36740
ID ABJ36740 standard; peptide; 11 AA.
XX
AC ABJ36740;
XX
DT 01-MAY-2003 (first entry)
XX
DE G protein coupled receptor related peptide SEQ ID NO 81.
XX
KW Nootropic; cardiant; antiarteriosclerotic; hypotensive; cytostatic;
KW antibacterial; analgesic; antiallergic; antiaesthetic; antiinflammatory;
KW osteoprotective; neuroprotective; anxiolytic; anorectic; lead compound;
KW G protein coupled receptor signaling inhibitor; GPCR; library;
KW high throughput screening assay; stroke; myocardial infarction;
KW restenosis; atherosclerosis; hypertension; cancer; infection; asthma;
KW septic shock; pain; allergic disorder; inflammatory bowel disease;
KW osteoporosis; obesity; psychotic; neurological disorder; anxiety;
KW schizophrenia; Alzheimer's disease.
XX
OS Caenorhabditis elegans.
XX
PN W0200272778-A2.
XX
PD 19-SEP-2002.
XX
PF 14-MAR-2002; 2002WO-US007561.
XX
PR 14-MAR-2001; 2001US-0275472P.
PR 11-MAY-2001; 2001US-00852910.
XX
PA (CUEB-) CUE BIOTECH.
XX
PI Gilchrist A, Hamm HE;
XX
DR WPI; 2003-247841/24.
XX
PT Identifying G protein coupled receptor (GPCR) signaling inhibitors,
PT useful in screening drugs for treating stroke, cancers or pain, by
PT identifying compounds that block GPCR mediated signaling with high
PT affinity and specificity.
XX
PS Claim 94; Page 25; 94pp; English.
XX
CC The invention relates to a novel method for identifying a G protein
CC coupled receptor (GPCR) signaling inhibitor. The novel method comprises
CC selecting or identifying a member of a library of peptides and/or
CC candidate compounds, having binding to a GPCR of higher affinity than
CC that of the native peptide. The peptide library is based on a native GPCR
CC binding peptide. The method is useful for identifying inhibitors of a G
CC protein coupled receptor (GPCR) signaling. The method is particularly
CC useful for identifying drugs that antagonise the binding between a GPCR
CC and its extracellular ligand(s). The method is especially useful in
CC modern high throughput screening assays for identifying potent lead
CC compounds. The compounds, peptides or inhibitors identified by the method
CC are useful for preventing, ameliorating or treating diseases in which
CC GPCR signaling is a causative factor or in which a specific class of G
CC protein is relevant, e.g. stroke, myocardial infarction, restenosis,
CC atherosclerosis, hypertension, cancers, infections, septic shock, pain,
CC allergic disorders, asthma, inflammatory bowel disease, osteoporosis,
CC obesity, or psychotic and neurological disorders (e.g. anxiety,
CC schizophrenia or Alzheimer's disease). This sequence represents a peptide
CC relating to the G protein coupled receptors of the invention
XX
SQ Sequence 11 AA;
XX

Query Match 36.1%; Score 26; DB 6; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.1e+03;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 5 VAKSVKSLYL 14
:|:|:|:|:
DB 1 IAKNLKSMGL 10

RESULT 42
ADT51155
ID ADT51155 standard; peptide; 11 AA.
XX
AC ADT51155;
XX
DT 13-JAN-2005 (first entry)
XX
DE G protein coupled receptor signalling modifying peptide #62.
XX
KW cerebroprotective; vasotropic; cardiant; antiarteriosclerotic;
KW hypotensive; cytostatic; antibacterial; fungicide; virocidic; analgesic;
KW antiallergic; antisthmatic; antiinflammatory; antiparkinsonian;
KW neuroprotective; nootropic; gene therapy; G protein coupled receptor;
KW GPCR; signaling modifying peptide; stroke; myocardial infarction;
KW atherosclerosis; hypertension; cancer; infection; pain; allergy; asthma;
KW inflammation; Parkinson's disease; Alzheimer's disease.
XX
OS Synthetic.
XX
PN W02004092199-A2.
XX
PD 28-OCT-2004.
XX
PF 12-APR-2004; 2004WO-US011167.
XX
PR 11-APR-2003; 2003US-00411336.
XX
PA (CUEB-) CUE BIOTECH INC.
XX
PI Gilchrist A, Hamm HM;
XX
DR WPI; 2004-766826/75.
XX
PT Identifying modulators of G protein coupled receptor (GPCR) signaling,
PT useful for treating diseases associated with altered GPCR signaling (e.g.
PT stroke) comprises screening a peptide library for high affinity binding
PT to the GPCR.
XX
PS Disclosure; SEQ ID NO 81; 264pp; English.
XX
CC The invention relates to a method of identifying a G protein coupled
CC receptor (GPCR) signaling modifying peptide by providing a peptide
CC library based on a native GPCR binding peptide, screening the peptide
CC library for high affinity binding to the GPCR, and selecting a member of
CC the peptide library having binding to the GPCR of higher affinity than
CC that of the native peptide. The composition and methods are useful for
CC identifying modulators of GPCR signaling, for modulating the activity of
CC GPCR or for drug designing. These may be used for diagnosing, preventing
CC or treating diseases associated with altered GPCR signaling, such as
CC stroke, myocardial infarction, atherosclerosis, hypertension, cancer,
CC infections (e.g. bacterial, fungal or viral), pain, allergies, asthma,
CC inflammation, Parkinson's disease and Alzheimer's disease. This sequence
CC corresponds to a peptide of the invention.
XX
SQ Sequence 11 AA;
XX

Query Match 36.1%; Score 26; DB 8; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.1e+03;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 5 VAKSVKSLYL 14
:|:|:|:|:
DB 1 IAKNLKSMGL 10

RESULT 43
AAR68663
ID AAR68663 standard; peptide; 12 AA.
XX
AC AAR68663;

```

XX 16-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 06-SEP-1995 (first entry)
XX
DE T cell epitope derived from V3 isolate SF2.
XX
KM T-cell; epitope; HIV-1; core protein; p24E; B-cell; antigen; gp160; gag;
KW pol; vaccine; multimeric peptide; AIDS; 3D organisation.
XX
OS Human immunodeficiency virus 1.
XX
PN WO9429339-A1.
XX
PD 22-DEC-1994.
XX
PF 08-JUN-1994; 94WO-CN000317.
XX
PR 09-JUN-1993; 93US-00073378.
XX
PA (CONN-) CONNAUGHT LAB LTD.
XX
PI Sia CDY, Chong P, Klein MH;
XX
DR WPI; 1995-036400/05.
XX
PT Novel tandem synthetic HIV-1 peptide(s) - comprising T-cell epitope of
PT gag protein linked to B-cell epitope of V3 loop protein of an HIV-1
XX isolate.
XX
PS Disclosure; Page 39; 69pp; English.
XX
CC This sequence represents a T-cell epitope derived from the V3 sequence of
CC the HIV-1 isolate SF2, which may be linked to a B-cell epitope from the
CC V3 (MN) loop from HIV-1. These chimeric peptides may then be used in the
CC production of HIV-1 vaccines. These peptide sequences may also be used in
CC the production of multimeric peptides in which the peptides are C-
CC terminally modified by the addition of a Lys residue which is modified on
CC its epsilon amino acid to carry an additional copy of the peptide
CC molecule. The linear and multimeric peptides may be used for the
CC treatment of AIDS by acting to displace the binding of HIV virus to human
CC or animal cells or by disturbing the 3D organisation of the virus.
CC (Updated on 25-MAR-2003 to correct PN field.) (Updated on 16-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 12 AA;
XX
Query Match 36.1%; Score 26; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 10 KSLYLIG 15
DB 2 KSIYIG 7
XX
RESULT 44
AAW25833
ID AAW25833 standard; peptide; 12 AA.
XX
AC AAW25833;
XX
DT 25-MAR-2003 (revised)
DT 20-OCT-1997 (first entry)
XX
DE HIV B-cell strain SF2 env protein V3 loop peptide.
XX
KM HIV; human immunodeficiency virus; gag; T-cell; B-cell; epitope; env;
KW V3 loop; vaccine; determinant; chimaeric.
XX
OS Synthetic.
XX
PN US5639854-A.

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XX 17-JUN-1997.
PD 09-JUN-1994; 94US-00257528.
XX
PF 09-JUN-1993; 93US-00073378.
XX
PR 09-JUN-1993; 93US-00073378.
XX
PA (CONN-) CONNAUGHT LAB LTD.
XX
PI Klein MH, Sia CDY, Chong P;
XX
DR WPI; 1997-332082/30.
XX
PT Tandem synthetic HIV peptide(s) useful as immunogens - comprising gag
PT protein T-cell epitope linked to env protein B-cell epitope.
XX
PS Disclosure; Col 21; 41pp; English.
XX
CC The invention relates to new synthetic peptides comprising at least one
CC amino acid sequence comprising an HIV gag protein T-cell epitope linked
CC at its C- or N-terminus to an amino acid sequence comprising a B-cell
CC epitope of the V3 loop of an HIV env protein, which can be used to
CC generate vaccines against HIV-1. The T-cell epitope sequence is pref.
CC selected from the T-helper determinant core peptides P24E, P24N, P24L,
CC P24M and P24H while the B-cell epitopes are derived from HIV strains
CC including CTLB-56, V3MN, CTLB-29, CTLB-55, SF2, LAI, IIB, RF, Z6, 2054,
CC 1714 and BX08. The peptides are chimaeric and can be linked to a branched
CC Lys backbone. This sequence represents the B-cell env protein V3 loop
CC peptide from HIV-1 strain SF2. (Updated on 25-MAR-2003 to correct PF
XX field.)
XX
SQ Sequence 12 AA;
XX
Query Match 36.1%; Score 26; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 10 KSLYLIG 15
DB 2 KSIYIG 7
XX
RESULT 45
AAW67349
ID AAW67349 standard; peptide; 12 AA.
XX
AC AAW67349;
XX
DT 17-OCT-2003 (revised)
DT 25-JAN-1999 (first entry)
XX
DE HIV-1 strain SF2 gp120 V3 loop epitope peptide.
XX
KM Immunogen; vaccine; HIV-1; T-cell; B-cell; epitope; core protein; gp120;
KW V3 loop.
XX
OS Human immunodeficiency virus 1.
XX
PN US5817754-A.
XX
PD 06-OCT-1998.
XX
PF 05-JUN-1995; 95US-00464329.
XX
PR 09-JUN-1993; 93US-00073378.
XX
PR 09-JUN-1994; 94US-00257528.
XX
PA (CONN-) CONNAUGHT LAB LTD.
XX
PI Chong P, Klein MH, Sia CDY;
XX
DR WPI; 1998-556461/47.
XX

```


PT Synthetic human immunodeficiency virus-1 peptide(s) - containing T-cell
PT epitope and B-cell epitope(s) are candidate vaccines against HIV-1.
XX
PS Disclosure; Col 21; 40pp; English.
XX
CC The invention relates to a novel immunogenic composition for use in
CC vaccines for the treatment of HIV-1 comprising an HIV-1-derived T-cell
CC epitope linked to an HIV-1-derived B-cell epitope. The T-cell epitopes
CC are generally designed based on the p24 core protein and the B-cell
CC epitopes from the V3 loop of the gp120 protein from various HIV-1
CC strains. This peptide represents the V3 loop epitope from the HIV-1
CC strain SF2. (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 12 AA;
XX
Query Match 36.1%; Score 26; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 10 KSLYLIG 15
||:|:
Db 2 KSIYIG 7
XX
RESULT 46
AAW99957
ID AAW99957 standard; peptide; 12 AA.
XX
AC AAW99957;
XX
DT 05-MAY-1999 (first entry)
XX
DE HIV-1 vaccine synthetic peptide SEQ ID NO:34.
XX
KM HIV-1; human immunodeficiency virus; vaccine; T-cell epitope;
XX gag protein; B-cell epitope; gp1 protein; chimeric; infection.
XX
OS Synthetic.
OS Human immunodeficiency virus 1.
XX
PN US5876731-A.
XX
PD 02-MAR-1999.
XX
PF 05-JUN-1995; 95US-00462507.
XX
PR 09-JUN-1993; 93US-00073378.
PR 09-JUN-1994; 94US-00257528.
XX
PA (CONN-) CONNAUGHT LAB LTD.
XX
PI Chong P, Klein MH, Sia CDY;
XX
DR WPI; 1999-189590/16.
XX
PT Synthetic chimeric HIV polypeptides - comprising gag protein T-cell
PT epitope linked to gp1 B-cell epitope.
XX
PS Example 1; Col 41-42; 41pp; English.
XX
CC The present invention describes a synthetic peptide comprising an amino
CC acid sequence containing a T-cell epitope of an HIV gag protein linked at
CC its C terminus to an amino acid sequence containing a B-cell epitope of
CC an HIV gp1 protein and containing the amino acid sequence: X1KDX2;
CC where X1 = E, A, G or Q, and X2 = A or T, or an amino acid sequence
CC capable of eliciting an HIV-specific antiserum and recognizing the
CC sequence X1KDX2. The synthetic peptide is useful in vaccines against
CC HIV infection and in diagnostic applications. AAW98892 to AAW98906, and
CC AAW98899 to AAW99989 represent synthetic peptides from the present
CC invention
XX
SQ Sequence 12 AA;

Query Match 36.1%; Score 26; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 10 KSLYLIG 15
||:|:
Db 2 KSIYIG 7
XX
RESULT 47
AAV39755
ID AAV39755 standard; peptide; 12 AA.
XX
AC AAV39755;
XX
DT 17-OCT-2003 (revised)
DT 26-NOV-1999 (first entry)
XX
DE HIV1 chimeric peptide V3-SF2.
XX
KM HIV; vaccine; immunogenic composition; T cell epitope; B cell epitope;
XX infection; antibody; antiviral.
XX
OS Human immunodeficiency virus 1.
OS
PN US5951966-A.
XX
PD 14-SEP-1999.
XX
PE 06-JUN-1995; 95US-00467881.
XX
PR 09-JUN-1993; 93US-00073378.
PR 09-JUN-1994; 94US-00257528.
XX
PA (CONN-) CONNAUGHT LAB LTD.
XX
PI Klein MH, Chong P, Sia CDY;
XX
DR WPI; 1999-550482/46.
XX
PT Immunogenic composition containing synthetic fusion polypeptides
PT containing both the T and B cell epitopes of the human immunodeficiency
PT virus, useful antigens in producing vaccines.
XX
PS Example 1; Col 22; 43pp; English.
XX
CC This sequence represents a fragment of a HIV1 protein, and can be used in
CC the immunogenic composition of the invention. The composition comprises a
CC synthetic fusion polypeptide which includes a sequence encoding 1 or more
CC T cell epitopes and a sequence encoding 1 or more B cell epitopes and a
CC carrier. Both the T cell and B cell epitopes are derived from HIV
CC proteins. The compositions are useful as vaccines against HIV infection.
CC The composition induces HIV-1-specific polyclonal antibodies that are
CC opsonising and antiviral. The peptide components may be selected to
CC induce a response against different viral isolates and in subjects who
CC recognise different T cell epitopes. (Updated on 17-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 12 AA;
XX
Query Match 36.1%; Score 26; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 10 KSLYLIG 15
||:|:
Db 2 KSIYIG 7
XX
RESULT 48
AAU70355
ID AAU70355 standard; peptide; 12 AA.
XX

XX 25-MAR-2004 (first entry)
XX Light chain CDR-1 peptide.
DE
XX
XX MUC1; mucin; cytosstatic; malignancy; cancer; CDR.
XX
XX Unidentified.
XX
XX WO2003106497-A1.
XX
XX 24-DEC-2003.
XX
XX 16-JUN-2003; 2003WO-GB002585.
XX
XX 14-JUN-2002; 2002US-0388313P.
XX
XX (IMMU-) IMMUNOMEDICS INC.
XX (MCCA/) MCCA L J D.
XX
XX Gold DV, Goldenberg DM, Hansen H;
XX WPI; 2004-156341/15.
XX
XX Novel tumor-associated PAM4 antibody binding a domain located between
PT amino terminus and start of repeat domain of MUC1, derived by
PT immunization and/or selection with mucin, useful for treating pancreatic
PT cancer.
XX
XX Claim 5; SEQ ID NO 1; 110pp; English.
XX
XX The present invention relates to an antibody or its fragment binding a
CC domain located between the amino terminus and the start of a repeat
CC domain of MUC1, derived by immunization and/or selection with mucin. The
CC method is useful for treating a malignancy in a subject, for delivering a
CC diagnostic/detection agent, a therapeutic agent, or its combination to a
CC target, for diagnosing or treating cancer, which involves administering
CC the antibody to a subject. The cancer is a pancreatic cancer. The method
CC can be used for intraoperative identification of diseased tissues,
CC endoscopic identification of diseased tissues or intravascular
CC identification of diseased tissues. The method is useful for treating a
CC cancer cell in a subject. The present sequence represents a complementary
CC determining region of the invention.
XX
XX Sequence 12 AA;
SQ
Query Match 36.1%; Score 26; DB 8; Length 12;
Best Local Similarity 54.5%; Pred. No. 1.2e+03;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 4 SVAKSVKSYL 14
| : | | | |
Db 1 SASSSVSSYL 11
RESULT 51
ADH59682
ID ADH59682 standard; peptide; 12 AA.
XX
XX ADH59682;
XX
XX 25-MAR-2004 (first entry)
XX
XX Light chain CDR1.
XX
XX PAM4 humanized; hPAM4; Cytostatic; Immunotherapy; cancer; CDR.
XX Homo sapiens.
XX
XX WO2003106495-A2.
XX
XX 24-DEC-2003.
XX

PF 16-JUN-2003; 2003WO-GB002593.
XX
XX 14-JUN-2002; 2002US-0388314P.
XX
XX (IMMU-) IMMUNOMEDICS INC.
XX (MCCA/) MCCA L J D.
XX
XX Goldenberg DM, Hansen H, Qu Z;
XX WPI; 2004-156340/15.
XX
XX Novel PAM4 humanized antibody or its fragment that binds to domain
PT located between amino terminus and start of repeat domain of MUC1, useful
PT for treating pancreatic cancer.
XX
XX Claim 6; SEQ ID NO 1; 109pp; English.
XX
XX The present invention relates to a PAM4 humanized (hPAM4) antibody or its
CC fragment that binds to the domain located between the amino terminus and
CC start of the repeat domain of MUC1, where the antibody is derived by
CC immunization and/or selection with mucin. The antibody is useful for
CC diagnosing or treating cancer, preferably pancreatic cancer, is useful
CC for treating a malignancy in a subject, is useful for treating a cancer
CC cell in a subject, is useful for detection of lesions during an
CC endoscopic, intravascular catheter, or surgical procedure, is also useful
CC for close-range lesion detection, during an operative, intravascular, or
CC endoscopic procedure. The antibody is efficiently useful in diagnosing
CC and treating pancreatic cancer. The present sequence represents a light
CC chain complementary determining region (CDR).
XX
XX Sequence 12 AA;
SQ
Query Match 36.1%; Score 26; DB 8; Length 12;
Best Local Similarity 54.5%; Pred. No. 1.2e+03;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 4 SVAKSVKSYL 14
| : | | | |
Db 1 SASSSVSSYL 11
RESULT 52
ADD90504
ID ADD90504 standard; protein; 14 AA.
XX
XX ADD90504;
XX
XX 29-JAN-2004 (first entry)
XX
XX Novel human secreted protein seq id 68 protein feature seq id 319.
XX gene therapy; cytosstatic; cancer; human; secreted protein.
XX Homo sapiens.
XX
XX US2003199683-A1.
XX
XX 23-OCT-2003.
XX
XX 30-MAR-2001; 2001US-00820649.
XX
XX 30-JUL-1997; 97US-0054209P.
XX 30-JUL-1997; 97US-0054212P.
XX 30-JUL-1997; 97US-0054212P.
XX 30-JUL-1997; 97US-0054213P.
XX 30-JUL-1997; 97US-0054215P.
XX 30-JUL-1997; 97US-0054217P.
XX 30-JUL-1997; 97US-0054218P.
XX 30-JUL-1997; 97US-0054234P.
XX 30-JUL-1997; 97US-0054236P.
XX 18-AUG-1997; 97US-0055968P.
XX 18-AUG-1997; 97US-0055969P.
XX

PR 18-AUG-1997; 97US-0055972P.
 PR 19-AUG-1997; 97US-0056534P.
 PR 19-AUG-1997; 97US-0056543P.
 PR 19-AUG-1997; 97US-0056554P.
 PR 19-AUG-1997; 97US-0056561P.
 PR 19-AUG-1997; 97US-0056727P.
 PR 19-AUG-1997; 97US-0056729P.
 PR 19-AUG-1997; 97US-0056730P.
 PR 29-JUL-1998; 98WO-US015949.
 PR 26-JAN-1999; 99US-00236557.
 PR 21-SEP-2000; 2000US-00666987.
 XX
 PA (RUBEN/) RUBEN S M.
 PA (FENG/) FENG P.
 PA (LAFLE/) LAFLEUR D W.
 PA (MOOR/) MOORE P A.
 PA (SHIY/) SHI Y.
 PA (KYAM/) KYAM H.
 PA (LIYI/) LI Y.
 PA (ZENG/) ZENG Z.
 PA (CART/) CARTER K C.
 PA (ENDR/) ENDRESS G A.
 PA (WEIY/) WEI Y.
 PA (FANP/) FAN P.
 PA (ROSE/) ROSEN C A.
 PI Ruben SM, Feng P, Lafleur DW, Moore PA, Shi Y, Kyaw H, Li Y;
 PI Zeng Z, Carter KC, Endress GA, Wei Y, Fan P, Rosen CA;
 XX
 DR WPI; 2003-852813/79.
 XX
 PT New nucleic acid molecule, useful for preparing a medicament for
 PT preventing, treating or ameliorating a medical condition e.g., cancer.
 XX
 PS Disclosure; SEQ ID NO 319; 213pp; English.
 XX
 CC The invention describes novel isolated human nucleic acids. The nucleic
 CC acid is useful for preparing a medicament for preventing, treating or
 CC ameliorating a medical condition e.g., cancer, and in gene therapy. This
 CC is the amino acid sequence of polypeptide feature of a novel human
 CC secreted protein of the invention.
 XX
 SQ Sequence 14 AA;
 XX
 QY 2 PFSVAKSV 9
 Db 3 PFSISYSI 10
 XX
 RESULT 53
 ADG90323
 ID ADG90323 standard; peptide; 14 AA.
 AC
 XX ADG90323;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Human secreted protein gene 58 extra polypeptide #1.
 XX
 KW Secretd protein; gene therapy; neural disorder; immune system disorders;
 KW muscular disorder; reproductive disorder; gastrointestinal disorder;
 KW pulmonary disorder; cardiovascular disorder; renal disorder;
 KW proliferative disorder; cancer; systemic lupus erythematosus;
 KW Rheumatoid arthritis; multiple sclerosis; thyroiditis; anaemia;
 KW Grave's disease; diabetes; hepatitis; asthma; allergy; nephritis;
 KW Parkinson's disease; Alzheimer's disease; atherosclerosis;
 KW myocardial infarction; AIDS; infection; human.
 XX
 OS Homo sapiens.

XX
 PN US200316541-A1.
 XX
 PD 04-SEP-2003.
 XX
 PF 04-JUN-2002; 2002US-00160162.
 XX
 PR 30-JUL-1997; 97US-0054209P.
 PR 30-JUL-1997; 97US-0054211P.
 PR 30-JUL-1997; 97US-0054212P.
 PR 30-JUL-1997; 97US-0054213P.
 PR 30-JUL-1997; 97US-0054214P.
 PR 30-JUL-1997; 97US-0054215P.
 PR 30-JUL-1997; 97US-0054217P.
 PR 30-JUL-1997; 97US-0054218P.
 PR 30-JUL-1997; 97US-0054234P.
 PR 30-JUL-1997; 97US-0054236P.
 PR 18-AUG-1997; 97US-0055688P.
 PR 18-AUG-1997; 97US-0055699P.
 PR 18-AUG-1997; 97US-0055972P.
 PR 19-AUG-1997; 97US-0056534P.
 PR 19-AUG-1997; 97US-0056543P.
 PR 19-AUG-1997; 97US-0056554P.
 PR 19-AUG-1997; 97US-0056561P.
 PR 19-AUG-1997; 97US-0056727P.
 PR 19-AUG-1997; 97US-0056729P.
 PR 19-AUG-1997; 97US-0056730P.
 PR 29-JUL-1998; 98WO-US015949.
 PR 26-JAN-1999; 99US-00236557.
 PR 05-JUN-2001; 2001US-0295558P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM, Feng P, Lafleur DW, Moore PA, Shi Y, Kyaw H, Li Y;
 PI Zeng Z, Carter KC, Endress GA, Wei Y, Fan P, Rosen CA;
 XX
 DR WPI; 2003-874923/81.
 XX
 PT Nucleic acids encoding 83 secreted polypeptides, useful for preventing,
 PT diagnosing and treating disorders related to their aberrant expression
 PT and activity.
 XX
 PS Disclosure; SEQ ID NO 319; 308pp; English.
 XX
 SQ
 XX
 CC The invention relates to an isolated nucleic acid molecule encoding a
 CC secreted protein that is at least 95% identical to a polynucleotide
 CC fragment of any of the nucleotide sequences listed in table 1A of the
 CC specification, which is hybridisable to the nucleotide sequences; a
 CC polynucleotide encoding a polypeptide (or a polypeptide fragment; a
 CC or epitope of any of the amino acid sequences) listed in table 1A of the
 CC specification, a polynucleotide which is an (allelic) variant of the
 CC nucleotide sequences listed in the specification, a polynucleotide which
 CC encodes a species homologue of the above amino acid sequences, a
 CC polynucleotide capable of hybridising under stringent conditions to any
 CC of the above polynucleotides, where the polynucleotide does not hybridise
 CC under stringent conditions to a nucleic acid molecule having a nucleotide
 CC sequence of only A or T residues. Also included are a recombinant vector
 CC comprising the above nucleic acid molecule, making a recombinant host
 CC cell comprising the above nucleic acid molecule, an isolated polypeptide
 CC comprising a sequence that is at least 95% identical to the polypeptide
 CC (or its fragment, domain, epitope, secreted form, (allelic) variant or
 CC homologue) encoded by the above nucleic acid molecule, an isolated
 CC antibody that binds specifically to the above polypeptide, a recombinant
 CC host cell produced by the above method and that expresses the above
 CC polypeptide, making an isolated polypeptide, preventing, treating or
 CC ameliorating a medical condition, diagnosing a pathological condition or
 CC a susceptibility to a pathological condition in a subject, identifying a
 CC binding partner to the above polypeptide, the gene corresponding to the
 CC cDNA sequence given in the specification, and identifying an activity in
 CC a biological assay. The nucleic acid molecule and polypeptide are useful
 CC in diagnosing, preventing, prognosing or treating diseases or disorders
 CC associated with aberrant expression and/or activity of the above
 CC polypeptide, such as neural disorders, immune system disorders, muscular

CC disorders, reproductive disorders, gastrointestinal disorders, pulmonary
CC disorders, cardiovascular disorders, renal disorders, proliferative
CC disorders and/or cancers. In particular, these diseases are systemic
CC lupus erythematosus, rheumatoid arthritis, multiple sclerosis
CC thyroiditis, anemia, Grave's disease, diabetes, hepatitis, asthma,
CC allergies, nephritis, Parkinson's disease, Alzheimer's disease,
CC atherosclerosis, myocardial infarction, AIDS and infections. The methods
CC may be used for identifying agonists and antagonists of the
CC polynucleotide and polypeptide. The present sequence is a protein from
CC one of the 83 disclosed secreted protein genes.
XX
SQ Sequence 14 AA:
Query Match 36.1%; Score 26; DB 7; Length 14;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 2 PFSVAKSV 9
|||:|:
Db 3 PFSISYSI 10
RESULT 54
ADU83344 standard; peptide; 14 AA.
XX
AC ADU83344;
XX
DT 10-FEB-2005 (first entry)
XX
DE NKkappa B-associated protein AD037 immunogenic peptide.
XX
XX Nucleic acid molecule encoding an NFkappaB associated molecule;
KM cardiovascular disease; neoplasia; gastrointestinal disease;
KM immune disorder; immune deficiency; dermatological disease; infection;
KM nutritional disorder; cerebrovascular ischemia; endocrine disease;
KM injury; respiratory disease; gynecology and obstetrics; Kawasaki disease;
KM rheumatic fever; diagnosis.
XX
XX Homo sapiens.
OS
XX WO2004100886-A2.
PN
XX 25-NOV-2004.
PD
XX 06-MAY-2004; 2004WO-US014279.
PF
XX 07-MAY-2003; 2003US-00431096.
PR
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
PA
XX Carman J, Feder JM, Nadler SG;
PI
XX WPI; 2005-047909/05.
DR
XX
XX New nucleic acid molecule encoding an NFkappaB associated molecule,
PT useful for diagnosing, preventing, treating, or ameliorating a medical
PT condition, e.g. cancer, wounds, or immune, inflammatory, hepatic, viral
PT or pulmonary disorder.
XX
XX Example 7; SEQ ID NO 289; 646bp; English.
XX
XX The invention relates to an isolated nucleic acid molecule having
CC NFkappaB (nuclear factor kappa B) modulating activity (or its fragments,
CC variants, homologs and sequences hybridizing to it). Also included are an
CC isolated polypeptide capable of modulating an NFkappaB response (or its
CC domain, epitope, variant, species homolog or interacting protein), an
CC isolated antibody that binds specifically to the isolated polypeptide, a
CC method for preventing (treating, or ameliorating) a medical condition, a
CC method of diagnosing a NFkappaB associated condition (or a susceptibility
CC to a NFkappaB associated condition) in a subject, a method for
CC identifying a binding partner to the polypeptide, a method of identifying
CC a compound that modulates the biological activity of a NFkappaB

CC associated molecule, a method of screening for a compound that is capable
CC of modulating the biological activity of a NFkappaB associated molecule
CC and a compound that modulates the biological activity of a human NFkappaB
CC associated molecule as identified by any of the methods above. The
CC nucleic acid molecule and polypeptides, composition and methods are
CC useful for diagnosing, preventing, treating, or ameliorating a medical
CC condition, e.g. immune disorder, an inflammatory disorder in which
CC polypeptides of the present invention are associated with the disorder
CC either directly or indirectly, an inflammatory disorder related to
CC aberrant NFkappaB regulation, a cancer, aberrant apoptosis, hepatic
CC disorders, Hodgkins lymphomas, hematopoietic tumors, hyper-IGM syndromes,
CC hypohydrotic ectodermal dysplasia, X-linked androdrotic ectodermal
CC dysplasia, immunodeficiency, albinism, influenza, viral
CC HIV-1, HTLV-1, hepatitis B, hepatitis C, EBV, influenza, viral
CC replication, host cell survival, and evasion of immune responses,
CC rheumatoid arthritis, inflammatory bowel disease, colitis, asthma,
CC atherosclerosis, cachexia, euthyroid sick syndrome, stroke, EAB,
CC autoimmune disorders, disorders related to hyper immune activity,
CC disorders related to aberrant acute phase responses, hypercongenital
CC conditions, birth defects, necrotic lesions, wounds, organ transplant
CC rejection, conditions related to organ transplant rejection, disorders
CC related to aberrant signal transduction, proliferating disorders, HIV
CC propagation in cells infected with other viruses, associated with EL-8,
CC disorders associated with aberrant IL-8 expression, disorders associated
CC with aberrant IL-8 activity, pulmonary disorders, pulmonary fibrosis,
CC Behcet's disease, bacterial infections, gynecological diseases,
CC psoriasis, IGA nephropathy, chronic obstructive pulmonary disease,
CC Kawasaki disease, Crohn's disease, peripheral arterial occlusive disease,
CC Hodgkin's disease, idiopathic intermediate uveitis, hyaline membrane
CC disease, acute rheumatic fever, chronic rheumatic heart disease,
CC ulcerative colitis, autoimmune disorders, and autoimmune thyroid disease.
CC The present sequence is an immunogenic peptide from the NFkappa B
XX modulating protein AD037.
XX
SQ Sequence 14 AA:
Query Match 36.1%; Score 26; DB 9; Length 14;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 VPFSVAKSVK 10
|||:|:
Db 1 VPISDSKSIQ 10
RESULT 55
ADY25663 standard; peptide; 14 AA.
ID
XX ADY25663;
XX
AC ADY25663;
XX
DT 05-MAY-2005 (first entry)
XX
XX Novel human secreted protein-related peptide SegID319.
DE
XX
XX cancer; cyrostatic; arthritis; antiarthritic; asthma; antiasthmatic;
KM acquired immune deficiency syndrome; rheumatoid arthritis; autoimmune;
KM inflammatory bowel disease; antiinflammatory; gastrointestinal-gen.;
KM sepsis; antibacterial; immunosuppressive; acne; antiseborrheic;
KM dermatological; psoriasis; antipsoriatic; atherosclerosis;
KM antiarteriosclerotic; cerebrovascular ischemia; cerebroprotective;
KM antiarteriosclerotic; wound healing; vulnery; Alzheimers disease;
KM vasoprotective; nocotropic; parkinsons disease; antiparkinsonian; autism;
KM obsessive-compulsive disorder; triquillizer; gift versus host disease;
KM immune disorder; hematological disease; inflammation; infection;
KM hyperproliferative disorders; renal disease; nephrotropic;
KM cardiovascular disease; cardiovascular-gen.; respiratory disorder;
KM neurological disease; neuroprotective; endocrine disease;
KM reproductive disorders (general); gynecological.
XX
XX Homo sapiens.
OS
XX US2005037467-A1.
PN

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XX 17-FEB-2005.
PD
XX
XX
PF 09-SEP-2004; 2004US-00936773.
XX
XX 30-JUL-1997; 97US-0054209P.
XX 30-JUL-1997; 97US-0054211P.
XX 30-JUL-1997; 97US-0054212P.
XX 30-JUL-1997; 97US-0054213P.
XX 30-JUL-1997; 97US-0054214P.
XX 30-JUL-1997; 97US-0054215P.
XX 30-JUL-1997; 97US-0054217P.
XX 30-JUL-1997; 97US-0054218P.
XX 30-JUL-1997; 97US-0054234P.
XX 30-JUL-1997; 97US-0054236P.
XX 18-AUG-1997; 97US-0055968P.
XX 18-AUG-1997; 97US-0055969P.
XX 18-AUG-1997; 97US-0055972P.
XX 19-AUG-1997; 97US-0056534P.
XX 19-AUG-1997; 97US-0056543P.
XX 19-AUG-1997; 97US-0056544P.
XX 19-AUG-1997; 97US-0056561P.
XX 19-AUG-1997; 97US-0056727P.
XX 19-AUG-1997; 97US-0056729P.
XX 19-AUG-1997; 97US-0056730P.
XX 29-JUL-1998; 98WO-US015949.
XX 26-JAN-1999; 99US-00236557.
XX 21-SEP-2000; 2000US-00666984.
XX 30-MAR-2001; 2001US-00820649.
XX 05-JUN-2001; 2001US-0295598P.
XX 04-JUN-2002; 2002US-00160162.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PI Ruben SM, Feng P, Lafleur DM, Moore PA, Shi Y, Kyaw H, Li Y;
PI Zeng Z, Carter KC, Endress GA, Wei Y, Fan P, Rosen CA;
XX
XX WPI; 2005-161941/17.
XX
XX PT New nucleic acid molecule encoding human secreted protein, useful for
XX PT preventing, treating, or ameliorating immune system, blood, inflammatory,
XX PT infectious, cardiovascular, respiratory, neurological, endocrine, or
XX PT reproductive disorders.
XX
XX PS Disclosure; SEQ ID NO 319; 309pp; English.
XX
XX CC The invention comprises the amino acid and coding sequences of novel
XX CC human secreted proteins and peptides. The DNA and protein sequences of
XX CC the invention are useful for treating or ameliorating: cancer, arthritis,
XX CC asthma, AIDS, rheumatoid arthritis, inflammatory bowel disease, sepsis,
XX CC acne, psoriasis, atherosclerosis, stroke, thrombosis, wound healing,
XX CC Alzheimer's Disease, Parkinson's Disease, autism, obsessive compulsive
XX CC disorder, graft-versus-host diseases, immune system disorders, blood
XX CC disorders, inflammatory conditions, infectious diseases.
XX CC hyperproliferative disorders, renal disorders, cardiovascular disorders,
XX CC respiratory disorders, neurological disorders, endocrine disorders, or
XX CC reproductive disorders. The present sequence is that of a human peptide
XX CC which is related to the novel human secreted proteins/peptides of the
XX CC invention.
XX
XX SQ Sequence 14 AA;

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Query Match 36.1%; Score 26; DB 9; Length 14;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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QY 2 PPSVAKSV 9
   |||::|:
Db 3 PFSISYSI 10

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RESULT 56
AEA36996

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ID AEA36996 standard; peptide; 14 AA.
XX
XX AEA36996;
AC
XX
XX 11-AUG-2005 (first entry)
DT
XX
XX DE Novel laminin binding site antimicrobial peptide SeqID21.
XX
XX KM antibacterial; fungicide; peptide therapy; bacterial infection;
XX KM fungal infection.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
FT Modified-site 14
FT /note="C-terminal amide"
XX
XX PN WO2005049819-A1.
XX
XX PD 02-JUN-2005.
XX
XX PF 25-OCT-2004; 2004WO-JP015803.
XX
XX PR 29-OCT-2003; 2003JP-00369595.
XX
XX PA (TOAG ) TOA GOSEI KK.
XX
XX PI Yoshida T, Yamada Y, Kume M, Kourai H;
XX PI WPI; 2005-396104/40.
XX
XX DR
XX
XX PT New artificially synthesized antimicrobial peptide capable of exerting an
XX PT antimicrobial property with respect to bacteria or fungi, useful for
XX PT treating bacterial infection and fungal infection.
XX
XX PS Claim 6; SEQ ID NO 21; 33pp; Japanese.
XX
XX CC This invention relates to a novel antimicrobial peptide capable of
XX CC exerting an antimicrobial property with respect to bacteria or fungi. The
XX CC peptide has a sequence comprising six consecutive amino acid residues
XX CC chosen from an amino acid sequence comprising a laminin-binding site
XX CC (LBS) or a sequence with amino acid substitutions in LBS, where the
XX CC peptide does not exist naturally, and is thus artificially synthesized.
XX CC The invention may be useful for the development of compounds with an
XX CC antibacterial or fungicide activity via peptide therapy. The peptides
XX CC effectively treat bacterial and fungal infections. The present sequence
XX CC is that of a novel antimicrobial peptide of the invention. Note: The
XX CC sequence listing does not form part of the written specification but was
XX CC obtained by the indexer in electronic format directly from WIPO.
XX
XX SQ Sequence 14 AA;

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```

Query Match 36.1%; Score 26; DB 9; Length 14;
Best Local Similarity 66.7%; Pred. No. 1.4e+03;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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```

QY 7 KSVKSLYLG 15
   | | | | |
Db 3 KKKRVLYLG 11

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RESULT 57
AEB18167
ID AEB18167 standard; peptide; 14 AA.
XX
XX AEB18167;
AC
XX
XX 22-SEP-2005 (first entry)
DT
XX
XX DE Prion disease-treatment peptide - SEQ ID 21.
XX
XX KW prion infection; cerebroprotective.
XX
XX

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OS	Unidentified.
XX	
PN	JP2005192415-A.
XX	
PD	21-JUL-2005.
XX	
PF	26-DEC-2003; 2003JP-00435425.
XX	
PR	26-DEC-2003; 2003JP-00435425.
XX	
PA	(TOAG) TOA GOSEI CHEM IND LTD.
XX	
PI	Yoshida T;
XX	
DR	WPI; 2005-501994/51.
XX	
PT	Novel non-natural peptide comprising amino acid residue of laminin
PT	coupling region, nuclear localization signal (NLS) and BIPARTITE NLS,
PT	useful for treating prion disease.
XX	
PS	Claim 6; SEQ ID NO 21; 36pp; Japanese.
XX	
CC	The invention comprises peptides which are useful for treating prion
CC	disease, the peptides of the invention contain at least six contiguous
CC	amino acid residues of a laminin coupling/bond region. The peptides of
CC	the invention are useful for treating prion disease. The present amino
CC	acid sequence represents a prion disease treatment peptide of the
CC	invention.
XX	
XX	Sequence 14 AA;
XQ	

Query Match	36.1%	Score 26	DB 9	Length 14
Best Local Similarity	66.7%	Pred. No. 1,4e+03		
Matches	6	conservative	0	Mismatches 3
				Indels 0
				Gaps 0
OY	7 KSVKSLYIG 15			
db	3 KKRRLVYIG 11			

RESULT 58
AAM12084
ID AAM12084 standard; peptide; 15 AA.
XX
AC AAM12084;
XX
DT 16-OCT-2003 (revised)
DT 02-APR-1997 (first entry)
XX
DE T-cell epitope peptide 126 from HIV sfz gp120.
KX
KW T-cell epitope; antigen; T-cell determinant; receptor; MHC protein; bird;
KM HIV sfz; herpes simplex virus; antigen gD2; tetanus toxoid; vaccine; HSV,
KV mammal; gp120; immune response; B-cell antigen.
XX
OS Human immunodeficiency virus 1.
XX
PN WO9518148-A1.
XX
PD 06-JUL-1995.
XX
PF 28-DEC-1993; 93WO-US011703.
XX
PR 28-DEC-1993; 93WO-US011703.
XX
PA (CHIR-) CHIRON MIMOTOPES PTY LTD.
XX
PI Geyssen HM, Rodda SJ;
XX
DR WPI, 1995-246333/32.
XX
PT T cell epitope peptide(s) - useful for detecting exposure of a subject to an antigen or pathogen, and in vaccines for birds and mammals.

XX Example 3; Page 18; 57pp; English.

PS

XX

CC AAM12069-W12086 represent a pool of T-cell epitope peptides created from

CC HIV sf2 gp120 (see AAM1977). This pool of epitopes also contains the

CC sequences represented by AAM1953-W1960. T-cell epitopes (also known as

CC T-cell determinants) are peptides (or regions of a protein) which bind to

CC T-cell antigen receptors in conjugation with MHC proteins. AAM1953-

CC W1976 were the most antigenic peptides obtained from the pools of

CC peptides created from the HIV sf2 gp120 (see AAM1953-W1960), herpes

CC simplex virus antigen gD2 (see AAM1961-W1969), and tetanus toxoid (see

CC AAM1970-W1976). These sequences can be used in methods for detecting

CC exposure of a mammal for bird to an antigen, and for increasing the number

CC of T-cells specific for an antigen. The peptides can also be used in a

CC method for determining T-cell epitopes specific for an antigen. These

CC methods allow for the identification of T-cell determinants. The T-cell

CC epitope peptides can be used in a vaccine for inducing an immune response

CC in a bird or mammal. The vaccine also contains a B-cell antigen,

CC preferably herpes simplex virus gD2 (see AAM12068) or HIV sf2 gp120 (see

CC AAM1977), and a carrier. (Updated on 16-OCT-2003 to standardise OS

CC field)

XX

XX

50 Sequence 15 AA;

```

Qy      10 KSLyLG 15
      |||:|
Db      8 KSLyIG 13

Query Match      36.1%; Score 26; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.6e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

CC	AA	Accession	Protein	Species	Source	Notes
XX	AA	AA11956	standard; peptide; 15 AA.	AA11956		
XX	AA	AA11956				
AC	AA	AA11956				
XX	DT	16-OCT-2003 (revised)				
DT	DT	02-APR-1997 (first entry)				
XX	DE	T-cell epitope #4 from HIV sf2 gp120.				
XX	KM	T-cell epitope; antigen; T-cell determinant; receptor; MHC protein; bird;				
KM	KM	HIV sf2; herpes simplex virus; antigen gp2; tetanus toxoid; vaccine; HSV;				
KW	KW	mammal; gp120; immune response; B-cell antigen.				
XX	OS	Human immunodeficiency virus 1.				
XX	XX	WO9518148-A1.				
XX	PD	06-JUL-1995.				
XX	PF	28-DEC-1993; 93WO-US011703.				
XX	PR	28-DEC-1993; 93WO-US011703.				
XX	PA	(CHIR-) CHIRON MIMOTOPES PTY LTD.				
XX	PI	Geysen HM, Rodda SJ;				
XX	DR	WPI; 1995-246333/32.				
XX	PT	T cell epitope peptide(s) - useful for detecting exposure of a subject to				
PT	PT	an antigen or pathogen, and in vaccines for birds and mammals.				
XX	PS	Claim 1; Page 45; 57pp; English.				
XX	AA	AA11953-W11976 represent T-cell epitope peptides. T-cell epitopes (also				
CC	CC	known as T-cell determinants) are peptides (or regions of a protein)				
CC	CC	which bind to T-cell antigen receptors in conjugation with MHC proteins.				
CC	CC	These sequences were the most antigenic peptides obtained from pools of				

CC peptides created from the HIV sf2 gp120 (AAW11953-W11960), herpes simplex
CC virus antigen gD2 (AAW11961-W11969), and tetanus toxoid (AAW11970-
CC W11976). These sequences can be used in methods for detecting exposure of
CC a mammal or bird to an antigen, and for increasing the number of T-cells
CC specific for an antigen. The peptides can also be used in a method for
CC determining T-cell epitopes specific for an antigen. These methods allow
CC for the identification of T-cell determinants. The T-cell epitope
CC peptides can be used in a vaccine for inducing an immune response in a
CC bird or mammal. The vaccine also contains a B-cell antigen, preferably
CC herpes simplex virus gD2 or HIV sf2 gp120 (see AAW11977), and a carrier.
CC (Updated on 16-OCT-2003 to standardise OS field)

XX
SQ Sequence 15 AA;

Query Match 36.1%; Score 26; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.6e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 KSLYLIG 15
||:|:
Db 2 KSIYIG 7

RESULT 60
AAW12086
ID AAW12086 standard; peptide, 15 AA.

XX AAW12086;
XX
AC 16-OCT-2003 (revised)
DT 02-APR-1997 (first entry)
XX
XX T-cell epitope peptide 128 from HIV sf2 gp120.
DE
XX
XX T-cell epitope; antigen; T-cell determinant; receptor; MHC protein; bird;
KW HIV sf2; herpes simplex virus; antigen gD2; tetanus toxoid; vaccine; HSV;
KW mammal; gp120; immune response; B-cell antigen.
XX
OS Human immunodeficiency virus 1.
XX
XX WO9518148-A1.
XX
XX 06-JUL-1995.
XX
XX 28-DEC-1993; 93WO-US011703.
XX
XX 28-DEC-1993; 93WO-US011703.
XX
XX (CHIR-) CHIRON MIMOTOPES PTY LTD.
XX
XX Geysen HM, Rodda SJ;
XX
XX WPI, 1995-246333/32.
XX
XX T cell epitope peptide(s) - useful for detecting exposure of a subject to
XX an antigen or pathogen, and in vaccines for birds and mammals.
XX
XX Example 3; Page 18; 57pp; English.

CC AAW12069-W12086 represent a pool of T-cell epitope peptides created from
CC HIV sf2 gp120 (see AAW11977). This pool of epitopes also contains the
CC sequences represented by AAW11953-W11960. T-cell epitopes (also known as
CC T-cell determinants) are peptides (or regions of a protein) which bind to
CC T-cell antigen receptors in conjugation with MHC proteins. AAW11953-
CC W11976 were the most antigenic peptides obtained from the pools of
CC peptides created from the HIV sf2 gp120 (see AAW11953-W11960), herpes
CC simplex virus antigen gD2 (see AAW11961-W11969), and tetanus toxoid (see
CC AAW11970-W11976). These sequences can be used in methods for detecting
CC exposure of a mammal or bird to an antigen, and for increasing the number
CC of T-cells specific for an antigen. The peptides can also be used in a
CC method for determining T-cell epitopes specific for an antigen. These
CC methods allow for the identification of T-cell determinants. The T-cell
CC epitope peptides can be used in a vaccine for inducing an immune response

CC in a bird or mammal. The vaccine also contains a B-cell antigen,
CC preferably herpes simplex virus gD2 (see AAW12068) or HIV sf2 gp120 (see
CC AAW11977), and a carrier. (Updated on 16-OCT-2003 to standardise OS
CC field)

XX
SQ Sequence 15 AA;

Query Match 36.1%; Score 26; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.6e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 KSLYLIG 15
||:|:
Db 4 KSIYIG 9

RESULT 61
AAW12085
ID AAW12085 standard; peptide, 15 AA.

XX AAW12085;
XX
AC 16-OCT-2003 (revised)
DT 02-APR-1997 (first entry)
XX
XX T-cell epitope peptide 127 from HIV sf2 gp120.
DE
XX
XX T-cell epitope; antigen; T-cell determinant; receptor; MHC protein; bird;
KW HIV sf2; herpes simplex virus; antigen gD2; tetanus toxoid; vaccine; HSV;
KW mammal; gp120; immune response; B-cell antigen.
XX
OS Human immunodeficiency virus 1.
XX
XX WO9518148-A1.
XX
XX 06-JUL-1995.
XX
XX 28-DEC-1993; 93WO-US011703.
XX
XX 28-DEC-1993; 93WO-US011703.
XX
XX (CHIR-) CHIRON MIMOTOPES PTY LTD.
XX
XX Geysen HM, Rodda SJ;
XX
XX WPI, 1995-246333/32.
XX
XX T cell epitope peptide(s) - useful for detecting exposure of a subject to
XX an antigen or pathogen, and in vaccines for birds and mammals.
XX
XX Example 3; Page 18; 57pp; English.

CC AAW12069-W12086 represent a pool of T-cell epitope peptides created from
CC HIV sf2 gp120 (see AAW11977). This pool of epitopes also contains the
CC sequences represented by AAW11953-W11960. T-cell epitopes (also known as
CC T-cell determinants) are peptides (or regions of a protein) which bind to
CC T-cell antigen receptors in conjugation with MHC proteins. AAW11953-
CC W11976 were the most antigenic peptides obtained from the pools of
CC peptides created from the HIV sf2 gp120 (see AAW11953-W11960), herpes
CC simplex virus antigen gD2 (see AAW11961-W11969), and tetanus toxoid (see
CC AAW11970-W11976). These sequences can be used in methods for detecting
CC exposure of a mammal or bird to an antigen, and for increasing the number
CC of T-cells specific for an antigen. The peptides can also be used in a
CC method for determining T-cell epitopes specific for an antigen. These
CC methods allow for the identification of T-cell determinants. The T-cell
CC epitope peptides can be used in a vaccine for inducing an immune response
CC in a bird or mammal. The vaccine also contains a B-cell antigen,
CC preferably herpes simplex virus gD2 (see AAW12068) or HIV sf2 gp120 (see
CC AAW11977), and a carrier. (Updated on 16-OCT-2003 to standardise OS
CC field)

XX
SQ Sequence 15 AA;

Query Match 36.1%; Score 26; DB 2; Length 15;
 Best Local Similarity 66.7%; Pred. No. 1.6e+03;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 KSLYLG 15
 ||:|:|
 DB 6 KSIYIG 11

RESULT 62

AAW12083
 ID AAW12083 standard; peptide; 15 AA.

XX AAW12083;
 XX
 DT 16-OCT-2003 (revised)
 DT 02-APR-1997 (first entry)
 XX
 DE T-cell epitope peptide 125 from HIV sf2 gp120.

XX
 KM T-cell epitope; antigen; T-cell determinant; receptor; MHC protein; bird;
 KM HIV sf2; herpes simplex virus; antigen gp2; tetanus toxoid; vaccine; HSV;
 KM mammal; gp120; immune response; B-cell antigen.

XX Human immunodeficiency virus 1.

PN MO9518148-A1.

XX 06-JUL-1995.

PF 28-DEC-1993; 93WO-US011703.

PR 28-DEC-1993; 93WO-US011703.

PA (CHIR-) CHIRON MIMOTOPES PTY LTD.

PI Geyesen HM, Rodda SJ;

DR WPI; 1995-246333/32.

PT T cell epitope peptide(s) - useful for detecting exposure of a subject to
 an antigen or pathogen, and in vaccines for birds and mammals.

PS Example 3; Page 18; 57pp; English.

CC AAW12069-W12086 represent a pool of T-cell epitope peptides created from
 CC HIV sf2 gp120 (see AAW11977). This pool of epitopes also contains the
 CC sequences represented by AAW1953-W1960. T-cell epitopes (also known as
 CC T-cell determinants) are peptides (or regions of a protein) which bind to
 CC T-cell antigen receptors in conjugation with MHC proteins. AAW1953-
 CC W1976 were the most antigenic peptides obtained from the pools of
 CC peptides created from the HIV sf2 gp120 (see AAW1953-W1960), herpes
 CC simplex virus antigen gp2 (see AAW1961-W1969), and tetanus toxoid (see
 CC AAW1970-W1976). These sequences can be used in methods for detecting
 CC exposure of a mammal or bird to an antigen, and for increasing the number
 CC of T-cells specific for an antigen. The peptides can also be used in a
 CC method for determining T-cell epitopes specific for an antigen. These
 CC methods allow for the identification of T-cell determinants. The T-cell
 CC epitope peptides can be used in a vaccine for inducing an immune response
 CC in a bird or mammal. The vaccine also contains a B-cell antigen,
 CC preferably herpes simplex virus gp2 (see AAW12069) or HIV sf2 gp120 (see
 CC AAW11977), and a carrier. (Updated on 16-OCT-2003 to standardise OS
 CC field)

XX
 SQ Sequence 15 AA;

Query Match 36.1%; Score 26; DB 2; Length 15;
 Best Local Similarity 66.7%; Pred. No. 1.6e+03;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 KSLYLG 15
 ||:|:|
 DB 10 KSIYIG 15

RESULT 63

AAW08008
 ID AAW08008 standard; peptide; 15 AA.

XX AAW08008;
 XX
 DT 16-OCT-2003 (revised)
 DT 03-FEB-1997 (first entry)
 XX
 DE V3 peptide #5.

XX HIV; gp120; HIV-IIIB strain; HIV-1 transmission; foetal transmission;
 KM neutralising antibody; passive immunisation; anti-idiotypic antibody;
 KM gp41; vaccine; active immunotherapy; V3.

XX Human immunodeficiency virus 1.

PN US556744-A.

PD 17-SEP-1996.

PF 24-MAR-1994; 94US-00218025.

PR 29-MAY-1992; 92US-00891451.

PA (UNIV-) UNIV PENNSYLVANIA.
 PA (WIST-) WISTAR INST ANATOMY & BIOLOGY.

PI Williams WV, Weiner DB, Ugen KE;

DR WPI; 1996-432980/43.

PT Determining the likelihood of maternal transmission of HIV-1 to foetus -
 PT by measuring maternal reactivity with specific gp120 and gp41 derived
 PT peptide(s), also used for diagnosing HIV in infants.

PS Disclosure; Col 109-110; 63pp; English.

XX AAW08004-W08015 represent HIV V3 peptides that can be used in the method
 CC of the invention. The method of the invention is for determining whether
 CC or not a mother will transmit HIV-1 to a foetus. The method comprises
 CC incubating a sample from the HIV-infected mother, with a collection of
 CC HIV peptides. The HIV peptides includes at least one gp41 derived peptide
 CC (see AAW07918-W07928), and at least one HIV gp120 derived peptide (see
 CC AAW07909-W07917). The number of peptides that react with the sample is
 CC determined, and this number is compared with a standard that shows
 CC pattern reactivity for a patient of transmission status. A non-
 CC transmissive HIV sample is indicated if the test sample reacts with twice
 CC as many peptides as the standard. The method detects the presence of
 CC neutralising antibodies that protect against mother to infant
 CC transmission of HIV. These sequences can also be used in vaccines to
 CC protect against transmission. Antibodies against these sequences can be
 CC used for passive immunisation, and to generate anti-idiotypic antibodies
 CC for use in vaccines or active immunotherapy. (Updated on 16-OCT-2003 to
 CC standardise OS field)

XX
 SQ Sequence 15 AA;

Query Match 36.1%; Score 26; DB 2; Length 15;
 Best Local Similarity 66.7%; Pred. No. 1.6e+03;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 KSLYLG 15
 ||:|:|
 DB 1 KSIYIG 6

RESULT 64

ABP30990
 ID ABP30990 standard; protein; 15 AA.
 XX

AC ABP30990;
XX
PF 02-JUL-2002 (first entry)
XX
DE Peptide #40 that corresponds to 0772P specific antibody epitope.
XX
KW Human; immunostimulant; cytostatic; cancer; ovarian carcinoma.
XX
OS Homo sapiens.
XX
PN WO200206317-A2.
XX
PD 24-JAN-2002.
XX
PF 17-JUL-2001; 2001WO-US022635.
XX
PR 17-JUL-2000; 2000US-00617747.
PR 10-AUG-2000; 2000US-00636801.
PR 20-SEP-2000; 2000US-00667857.
PR 04-APR-2001; 2001US-00827271.
PR 18-JUN-2001; 2001US-00884441.
XX
PA (CORI-) CORIXA CORP.
XX
PI Mitcham JL, King GE, Algate PA, Fling SP, Retter MW, Fanger GR;
PI Reed SG, Vedvick TS, Carter D, Hill P, Albone E;
XX
DR WPI; 2002-164781/21.
XX
PT Polypeptides comprising an immunogenic portion of an ovarian carcinoma
PT protein or its variants, useful for stimulating an immune response in a
PT patient and treating ovarian cancer.
XX
PS Claim 33; Page 364; 408pp; English.
XX
CC This invention relates to polypeptides comprising an immunogenic portion
CC of an ovarian carcinoma protein which acts as an immunostimulant and is
CC cytostatic. The polypeptides, polynucleotides, antibodies, fusion
CC proteins, T cell populations and antigen presenting cells that express
CC the polypeptides are useful for stimulating an immune response in a
CC patient and treating ovarian cancer. This sequence represents protein
CC related to the invention
XX
SQ Sequence 15 AA;

Query Match 36.1%; Score 26; DB 5; Length 15;
Best Local Similarity 53.8%; Pred. No. 1.6e+03;
Matches 7; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY 2 PPSVAKSVKSLYL 14
|:|:|:|
Db 2 PYSLDKD--SLYL 12

RESULT 65
ABP56426
ID ABP56426 standard; peptide; 15 AA.
XX
AC ABP56426;
XX
DT 13-MAR-2003 (first entry)
XX
DE Human scorpion short chain toxic protein 18.59 peptide SEQ ID NO:7.
XX
KW Human; scorpion short chain toxic protein 18.59; malignant tumour;
KW haemopathy; human immunodeficiency virus infection; HIV infection;
KW immunological disease; inflammation.
XX
OS Homo sapiens.
XX
PN CN1352108-A.
XX
PD 05-JUN-2002.

XX
XX 06-NOV-2000; 2000CN-00127238.
XX
PR 06-NOV-2000; 2000CN-00127238.
XX
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-692404/75.
XX
PT New human scorpion short chain toxin protein 18.59 polypeptide for
PT treating malignant tumors, hemopathy, human immunodeficiency virus
PT infection, immunological diseases and various inflammations.
XX
PS Example 5; Page 18 (Disclosure); 33pp; Chinese.
XX
CC The present invention describes human scorpion short chain toxin protein
CC 18.59 (I). Also described is a DNA recombination process used to produce
CC (I). (I) can be used for treating various diseases, such as malignant
CC tumours, haemopathy, human immunodeficiency virus (HIV) infection,
CC immunological diseases and various inflammations. The present sequence
CC represents the N-terminal peptide of (I), which is used in an example
CC from the present invention
XX
SQ Sequence 15 AA;

Query Match 36.1%; Score 26; DB 5; Length 15;
Best Local Similarity 36.4%; Pred. No. 1.6e+03;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 PPSVAKSVKSL 12
|:|:|:|
Db 3 PYQILKAQKAL 13

RESULT 66
ADA08653
ID ADA08653 standard; peptide; 15 AA.
XX
AC ADA08653;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human 0772P-specific antibody epitope #11.
XX
KW epitope; human; gene therapy; ovarian cancer; cancer.
XX
OS Homo sapiens.
XX
PN US2003091580-A1.
XX
PD 15-MAY-2003.
XX
PF 17-JUL-2001; 2001US-00907969.
XX
PR 18-JUN-2001; 2001US-00884441.
XX
PA (MITC/) MITCHAM J L.
PA (KING/) KING G E.
PA (ALGA/) ALGATE P A.
PA (FLIN/) FLING S P.
PA (RETT/) RETTER M W.
PA (FANG/) FANGER G R.
PA (REED/) REED S G.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (HILL/) HILL P.
PA (ALBO/) ALBONE E.
XX
PI Mitcham JL, King GE, Algate PA, Fling SP, Retter MW, Fanger GR;
PI Reed SG, Vedvick TS, Carter D, Hill P, Albone E;

PS Example 15; SEQ ID NO 500; 399pp; English.

CC Note the epitope sequences are displayed in tables VII-XLIX.

SQ Sequence 15 AA;

Query Match 36.1%; Score 26; DB 8; Length 15;
Best Local Similarity 58.3%; Pred. No. 1.6e+03;
Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 FSVAKSVKSLYL 14
|||
Db 4 FSSQKGVKGLPL 15

RESULT 69

ADN94644
ID ADN94644 standard; peptide; 15 AA.

AC ADN94644;

DT 01-JUL-2004 (first entry)

DE Human 202P5A5v.1 protein epitope #4880.

XX 202P5A5; human; cancer; tumour; epitope.

XX Homo sapiens.

XX WO2004016736-A2.

XX 26-FEB-2004.

XX 16-JUN-2003; 2003WO-US018906.

XX 16-AUG-2002; 2002US-0404306P.

XX 01-NOV-2002; 2002US-0423290P.

XX (AGEN-) AGENSYS INC.

XX Raitano AB, Faris M, Challita-Eid PM, Jakobovits A, Ge W;

DR WPI; 2004-203774/19.

New compositions having the 202P5A5 gene and encoded protein, useful for
diagnosing, preventing, prognosticating or treating cancer of the
prostate, bladder, colon, lung, ovary, breast, stomach, cervix, lymphoma,
bone and/or skin.

PS Claim 1; Fig 2A; 266bp; English.

The invention relates to a composition comprising 202P5A5 proteins. The
composition and proteins are useful for detecting and treating cancer by
inhibiting the growth or viability of cancer cells. The present sequence
represents the amino acid sequence of a human 202P5A5v.1 protein epitope.
Note the epitope sequences are displayed in tables VIII-XLIX.

SQ Sequence 15 AA;

Query Match 36.1%; Score 26; DB 8; Length 15;
Best Local Similarity 58.3%; Pred. No. 1.6e+03;
Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 FSVAKSVKSLYL 14
|||
Db 2 FSSQKGVKGLPL 13

RESULT 70

ADN94062
ID ADN94062 standard; peptide; 15 AA.

AC ADN94062;

DT 01-JUL-2004 (first entry)

DE Human 202P5A5v.1 protein epitope #4298.

XX 202P5A5; human; cancer; tumour; epitope.
XX Homo sapiens.

XX WO2004016736-A2.

XX 26-FEB-2004.

XX 16-JUN-2003; 2003WO-US018906.

XX 16-AUG-2002; 2002US-0404306P.

XX 01-NOV-2002; 2002US-0423290P.

XX (AGEN-) AGENSYS INC.

XX Raitano AB, Faris M, Challita-Eid PM, Jakobovits A, Ge W;

DR WPI; 2004-203774/19.

New compositions having the 202P5A5 gene and encoded protein, useful for
diagnosing, preventing, prognosticating or treating cancer of the
prostate, bladder, colon, lung, ovary, breast, stomach, cervix, lymphoma,
bone and/or skin.

PS Claim 1; Fig 2A; 266bp; English.

The invention relates to a composition comprising 202P5A5 proteins. The
composition and proteins are useful for detecting and treating cancer by
inhibiting the growth or viability of cancer cells. The present sequence
represents the amino acid sequence of a human 202P5A5v.1 protein epitope.
Note the epitope sequences are displayed in tables VIII-XLIX.

SQ Sequence 15 AA;

Query Match 36.1%; Score 26; DB 8; Length 15;
Best Local Similarity 58.3%; Pred. No. 1.6e+03;
Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 FSVAKSVKSLYL 14
|||
Db 4 FSSQKGVKGLPL 15

RESULT 71

ADN94078
ID ADN94078 standard; peptide; 15 AA.

AC ADN94078;

DT 01-JUL-2004 (first entry)

DE Human 202P5A5v.1 protein epitope #4314.

XX 202P5A5; human; cancer; tumour; epitope.

XX Homo sapiens.

XX WO2004016736-A2.

XX 26-FEB-2004.

XX 16-JUN-2003; 2003WO-US018906.

XX 16-AUG-2002; 2002US-0404306P.

XX 01-NOV-2002; 2002US-0423290P.

XX (AGEN-) AGENSYS INC.

XX Raitano AB, Faris M, Challita-Eid PM, Jakobovits A, Ge W;

DR WPI; 2004-203774/19.

PT New compositions having the 202PSA5 gene and encoded protein, useful for
PT diagnosing, preventing, prognosticating or treating cancer of the
PT prostate, bladder, colon, lung, ovary, breast, stomach, cervix, lymphoma,
XX bone and/or skin.
XX
PS Claim 1; Fig 2A; 266pp; English.
XX
CC The invention relates to a composition comprising 202PSA5 proteins. The
CC composition and proteins are useful for detecting and treating cancer by
CC inhibiting the growth or viability of cancer cells. The present sequence
CC represents the amino acid sequence of a human 202PSA5v.1 protein epitope.
CC Note the epitope sequences are displayed in tables VIII-XLIX.
XX
SQ Sequence 15 AA;
XX
Query Match 36.1%; Score 26; DB 8; Length 15;
Best Local Similarity 58.3%; Pred. No. 1.6e+03;
Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 3 FSVAKSVKSLYL 14
Db 1 FSSQKGVKGLPL 12
XX
RESULT 72
AD17879
ID ADX17879 standard; peptide; 15 AA.
XX
AC ADX17879;
XX
DT 21-APR-2005 (first entry)
XX
DE Human ovarian carcinoma antigen O772P antibody epitope #11.
XX
KM diagnosis; cytostatic; immunostimulant; gene therapy; tumor;
KM ovarian tumor; cancer; carcinoma; antigen.
XX
OS Homo sapiens.
XX
PN US2005031634-A1.
XX
PD 10-FEB-2005.
XX
PF 02-JUN-2004; 2004US-00860790.
XX
PR 17-DEC-1998; 98US-00216003.
PR 23-JUN-1999; 99US-00338933.
PR 24-SEP-1999; 99US-00404879.
PR 17-JUL-2000; 2000US-00617747.
PR 10-AUG-2000; 2000US-00636801.
PR 20-SEP-2000; 2000US-00667857.
PR 04-APR-2001; 2001US-00827271.
PR 18-JUN-2001; 2001US-00884441.
PR 17-JUL-2001; 2001US-00907969.
PR 17-JUL-2002; 2002US-00198053.
XX
PA (CORI-) CORIXA CORP.
XX
PI Bangur CS, Rector MW, Fanger GR, Hill P;
XX
DR WPI; 2005-151645/16.
XX
PT New ovarian carcinoma polynucleotides, preferably cDNAs, useful for
PT diagnosing, preventing and treating diseases, such as ovarian cancer, and
PT for eliciting humoral and/or cellular immune response.
XX
PS Example 15; SEQ ID NO 500; 398pp; English.
XX
CC The invention relates to an isolated polynucleotide comprising a sequence
CC of a sequence hybridizing under highly stringent conditions to, or
CC having at least 75, or 90% identity to a 849 or 1399 bp, fully defined in
CC the specification, its complement or degenerate variants, or a sequence
CC of at least 20 contiguous residues of the 849 or 1399 bp sequence. The

CC polynucleotides and polypeptides are useful for diagnosing, preventing
CC and treating diseases, such as ovarian cancer, and for eliciting humoral
CC and/or cellular immune response. This sequence corresponds to an ovarian
CC carcinoma antigen peptide of the invention.
XX
SQ Sequence 15 AA;
XX
Query Match 36.1%; Score 26; DB 9; Length 15;
Best Local Similarity 53.8%; Pred. No. 1.6e+03;
Matches 7; Conservative 2; Mismatches 2; Indels 2; Gaps 1;
OY 2 PFSVAKSVKSLYL 14
Db 2 PYSIDKD--SLYL 12
XX
RESULT 73
ADM19018
ID ADM19018 standard; peptide; 14 AA.
XX
AC ADM19018;
XX
DT 17-JUN-2004 (first entry)
XX
DE HLA-DR bound peptide SEQ ID NO:53.
XX
KM antigenic peptide; cytostatic; anti-HIV; virucide; hepatotropic;
KM antiinflammatory; antibacterial; antidiabetic; antineumatic;
KM antiarthritic; immunosuppressive; neuroprotective; dermatological;
KM vaccine; T cell activator; cancer; melanoma; breast cancer;
KM B cell lymphoma; prostate cancer; renal cancer; infectious disease; HIV;
KM hepatitis C virus; measles virus; mycobacteria; autoimmune disease;
KM rheumatoid arthritis; type I diabetes; multiple sclerosis;
KM myaschena gravis; systemic lupus erythematosus; HLA-DR bound peptide.
XX
OS Homo sapiens.
XX
PN EP1405862-A2.
XX
PD 07-APR-2004.
XX
PF 24-SEP-2003; 2003EP-00021521.
XX
PR 02-OCT-2002; 2002EP-00022223.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Kropshofer H, Vogt A;
XX
DR WPI; 2004-318705/30.
XX
PT Isolating antigenic peptides in femtomolar amounts, comprises providing
PT complexes of peptide receptors with antigenic peptides isolated from
PT mammalian organism, and eluting associated antigenic peptides from
PT peptide receptors.
XX
PS Example 4; SEQ ID NO 53; 51pp; English.
XX
CC The present invention describes a method (M1) for isolating antigenic
CC peptides (I) in femtomolar amounts, by providing complexes of peptide
CC receptors with (I) isolated from mammal, and eluting associated (I) from
CC peptide receptors, or providing complexes of peptide receptors with (I)
CC isolated from cell or tissue of mammal, washing sequestered complexes of
CC peptide receptors with (I), eluting associated (I) from peptide
CC receptors, sequencing and identifying isolated peptides. Also described
CC is a method for producing a pharmaceutical composition (II), which
CC involves carrying out the steps of (M1), producing the identified
CC peptides and optionally modifying them, and formulating the product
CC obtained with a carrier or diluent (I) and (II) have cytostatic, anti-
CC HIV, virucide, hepatotropic, antiinflammatory, antibacterial,
CC antidiabetic, antineumatic, antiarthritic, immunosuppressive,
CC neuroprotective and dermatological activities, and can be used in
CC vaccines and as activators of T cells. (M1) is useful for isolating

CC	antigenic peptides in femtomolar amounts, from a mammal such as human.
CC	(M1) is useful for quality control of vaccines, immune monitoring of
CC	diseases, control of the efficacy of a therapeutic treatment and design
CC	of individualised peptide vaccines for the treatment of diseases. (M1) is
CC	also useful for producing a pharmaceutical composition. The peptides
CC	identified by (M1) are useful in vaccinating patients against cancer such
CC	as melanoma, breast cancer, B cell lymphoma, prostate cancer and renal
CC	cancer, infectious diseases such as diseases caused by HIV, hepatitis C
CC	virus, measles virus and mycobacteria, and autoimmune diseases such as
CC	rheumatoid arthritis, type I diabetes, multiple sclerosis, myasthenia
CC	gravis and systemic lupus erythematosus. The present sequence represents
CC	an HLA-DR bound peptide, which is used in an example from the present
CC	invention.
CC	
XX	
SQ	Sequence 14 AA;
Query Match	35.4%; Score 25.5; DB 8; Length 14;
Best Local Similarity	50.0%; Pred. No. 1.8e+03;
Matches	6; Conservative 4; Mismatches 1; Indels 1; Gaps 1
QY	4 SVAKSVKSL-YL 14 : ::
Db	2 AVKSIKSIPIYL 13
RESULT 74	
ADMI9019	
ID	ADMI9019 standard; peptide; 15 AA.
XX	
AC	ADMI9019;
XX	
DT	17-JUN-2004 (first entry)
XX	
DE	HLA-DR bound peptide SEQ ID NO:54.
XX	
KW	antigenic peptide; cytostatic; anti-HIV, virucide; hepatotropic;
KW	antiinflammatory; antibacterial; antidiabetic; antirheumatic;
KW	antiarthritic; immunosuppressive; neuroprotective; dermatological;
KW	vaccine; T cell activator; cancer; melanoma; breast cancer;
KW	B cell lymphoma; prostate cancer; renal cancer; infectious disease; HIV;
KW	hepatitis C virus; measles virus; mycobacteria; autoimmune disease;
KW	rheumatoid arthritis; type I diabetes; multiple sclerosis;
KW	myasthenia gravis; systemic lupus erythematosus; HLA-DR bound peptide.
XX	
OS	Homo sapiens.
XX	
PN	EPI405862-A2.
XX	
PD	07-APR-2004.
XX	
PF	24-SEP-2003; 2003EP-00021521.
XX	
PR	02-OCT-2002; 2002EP-00022223.
XX	
PA	(HOFF) HOFFMANN LA ROCHE & CO AG F.
XX	
P1	Kropshofer H, Vogt A;
XX	
WI	WPI; 2004-318705/30.
DR	
XX	
PT	Isolating antigenic peptides in femtomolar amounts, comprises providing
PT	complexes of peptide receptors with antigenic peptides isolated from
PT	mammalian organism, and eluting associated antigenic peptides from
PT	peptide receptors.
XX	
PS	Example 4; SEQ ID NO 54; Sipp; English.
XX	
CC	The present invention describes a method (M1) for isolating antigenic
CC	peptides (I) in femtomolar amounts, by providing complexes of peptide
CC	receptors with (I) isolated from mammal, and eluting associated (I) from
CC	peptide receptors, or providing complexes of peptide receptors with (I)
CC	isolated from cell or tissue of mammal, washing sequestered complexes of
CC	peptide receptors with (I), eluting associated (I) from peptide

CC	receptors, sequencing and identifying isolated peptides. Also described
CC	is a method for producing a pharmaceutical composition (II), which
CC	involves carrying out the steps of (M1), producing the identified
CC	peptides and optionally modifying them, and formulating the product
CC	obtained with a carrier or diluent. (I) and (II) have cytostatic, anti-
CC	HIV, virinide, hepatotropic, antiinflammatory, antibacterial,
CC	antidiabetic, antineumatic, antiarthritic, immunosuppressive,
CC	neuroprotective and dermatological activities, and can be used in
CC	vaccines and as activators of T cells. (M1) is useful for isolating
CC	antigenic peptides in femomolar amounts, from a mammal such as human.
CC	(M1) is useful for quality control of vaccines, immune monitoring of
CC	diseases, control of the efficacy of a therapeutic treatment and design
CC	of individualised peptide vaccines for the treatment of diseases. (M1) is
CC	also useful for producing a pharmaceutical composition. The peptides
CC	identified by (M1) are useful in vaccinating patients against cancer such
CC	as melanoma, breast cancer, B cell lymphoma, prostate cancer and renal
CC	cancer, infectious diseases such as diseases caused by HIV, hepatitis C
CC	virus, measles virus and mycobacteria, and autoimmune diseases such as
CC	rheumatoid arthritis, type 1 diabetes, multiple sclerosis, myasthenia
CC	gravis and systemic lupus erythematosus. The present sequence represents
CC	an HLA-DR bound peptide, which is used in an example from the present
CC	invention.
CC	
CC	
SQ	Sequence 15 AA:
QY	4 SVASVSVSL-YL 14 : ::: : 3 AVVKSIRSIPTL 14
Db	
RESULT 75	
AA777393	
ID	AA777393 standard; peptide; 8 AA.
AC	AA777393;
XX	22-MAY-2000 (first entry)
DE	HIV-1 group O env epitope, SEQ ID NO:109.
XX	
KW	HIV-1 group O; env; gp120; gp41; glycoprotein; monoclonal antibody;
KW	immunoassay; positive control; affinity purification; therapeutic;
KM	Escherichia coli; reactive; epitope.
XX	
OS	Human immunodeficiency virus 1; group O.
OS	Synthetic.
XX	
PN	WO200004383-A2.
PD	27-JAN-2000.
XX	
PF	09-JUL-1999; 99WO-US015469.
PR	14-JUL-1998; 98US-00115171.
XX	
PA	(ABBO) ABBOTT LAB.
XX	
PI	Scheffel JW, Hackett JR, Tyner JD, Hickman RK;
DR	WPI; 2000-171290/15.
XX	
PT	Novel monoclonal antibodies useful as positive control reagent for
PT	detecting human immunodeficiency virus infections and diagnosing,
PT	evaluating or prognosing viral disease.
XX	
ES	Claim 18; Page 70; 148pp; English.
CC	The invention relates to anti-HIV-1 group O monoclonal antibodies, which
CC	may be used as positive control reagents in immunoassays to detect and

CC differentiate HIV-1 infections. The invention also encompasses a
CC monoclonal antibody which binds specifically to an HIV-1 group O antigen,
CC which has no more than 15% cross reactivity to a corresponding antigen
CC selected from HIV-1 group M antigens and HIV-2 antigens; and a method of
CC using a monoclonal antibody as a positive control reagent in an
CC immunoassay for the detection of anti HIV-1 group O antibodies. The
CC monoclonal antibodies are useful as positive control reagents in
CC immunoassays capable of detecting anti-HIV-1 Group O antibodies. Such
CC immunoassays involve coupling a monoclonal antibody with HIV group-1
CC antigen and detecting the antigen-antibody complex. The monoclonal
CC antibodies of the invention would be used to ensure that the reagents
CC provided to detect HIV-1 group O antibody were performing properly. The
CC monoclonal antibodies may also be immobilised on a matrix and used
CC for affinity purification of specific HIV-1 group O-derived proteins from
CC cell cultures or biological tissues. The monoclonal antibodies can also
CC be used for generating chimeric antibodies for therapeutic use. Different
CC epitopes of HIV antigens can be used in combination in assay to diagnose,
CC evaluate, or prognosticate HIV disease condition. The monoclonal
CC antibodies are also useful for differentiating HIV-1 Group O antigens
CC from HIV-group M and HIV-2 antigens. Sequences AAY77389-Y77398 represent
CC HIV-1 group O env epitopes
XX
SQ Sequence 8 AA;

Query Match 34.7%; Score 25; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PFSVA 6
Db 1 PFSVA 5
|||||
1 PFSVA 5

RESULT 76
ABB76741
ID ABB76741 standard; peptide; 8 AA.
XX
XX ABB76741;
AC
XX
DT 31-MAY-2002 (first entry)
XX
DE Tumour antigen epitope gp102029 presented by HLA A2.1.
XX
XX Antiviral; anti-HIV; cytostatic; epitope; HLA A2.1;
KM human leukocyte antigen; immunotherapy; cancer; viral infection; vaccine.
XX
XX Unidentified.
OS
XX FR2812087-A1.
PN
XX PD 25-JUN-2002.
XX
XX PF 21-JUL-2000; 2000FR-00009591.
XX
XX PR 21-JUL-2000; 2000FR-00009591.
XX
XX PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX
XX PI Kosmatopoulos K, Tourdot S, Scardino A, Gross DA;
XX DR WPI; 2002-189846/25.
XX
XX PT Identifying subdominant or cryptic epitopes, useful in immunotherapy of
XX cancer and viral infection, comprises testing modified, non-immunogenic
XX peptides for induction of cytotoxic T cells.
XX
XX PS Example 1; Page 12; 62pp; French.
XX
XX CC The present invention relates to subdominant/cryptic epitopes that are
XX presented by HLA (human leukocyte antigen) Class I molecule A2.1. The
XX epitopes or chimeric polypeptides containing them and nucleic acid
XX encoding them are useful for preventative or curative immunotherapy of

CC cancer and viral infections, particularly where used as vaccines. The
CC present peptide was used to illustrate the invention
XX
SQ Sequence 8 AA;

Query Match 34.7%; Score 25; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSV 5
Db 4 VPFSV 8
|||||
4 VPFSV 8

RESULT 77
ADH62104
ID ADH62104 standard; peptide; 8 AA.
XX
XX ADH62104;
AC
XX DT 25-MAR-2004 (first entry)
XX
XX Cyclic antiviral peptide, SEQ ID NO:83.
XX
XX Antiviral peptide; prophylaxis; therapy; drug screening; virucide;
KM hepatotropic; antiinflammatory; vaccine; cyclic.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH MISC-difference 2 /note= "D-form residue"
FT MISC-difference 4 /note= "D-form residue"
FT MISC-difference 6 /note= "D-form residue"
FT MISC-difference 8 /note= "D-form residue"
FT MISC-difference 8 /note= "D-form residue"
XX
XX W02003092631-A2.
XX
XX PN 13-NOV-2003.
XX
XX PD 06-MAY-2003; 2003WO-US014372.
XX
XX PF 06-MAY-2002; 2002US-0378256P.
XX
XX PR (SCRI) SCRIPPS RES INST.
XX
XX PA Ghadiri MR;
XX
XX PI WPI; 2004-042365/04.
XX
XX DR
XX
XX PT New fast-acting cyclic peptide anti-viral agents that do not cause
XX undesired lysis of animal cells, useful for the preparation of a
XX medicament for the prevention and/or treatment of viral infections.
XX
XX PS Example 2; SEQ ID NO 83; 23pp; English.
XX
XX
XX CC The invention relates to cyclic antiviral peptides which do not cause
XX undesired lysis of animal cells. The cyclic peptides are composed of 4-16
XX alternating L- and D-form amino acids. The invention also relates to use
XX of the cyclic peptides for treating and preventing viral infection,
XX particularly adenoviral infection, in an animal; pharmaceutical
XX compositions comprising a peptide of the invention; and methods for
XX identifying or evaluating a cyclic peptide with anti-viral activity. The
XX peptides are substantially non-toxic to mammals and may be used to treat
XX or prevent infection by a wide variety of viruses. These viruses include:
XX hepatitis A virus (HAV), hepatitis B virus (HBV), hepatitis C virus
XX (HCV), human immunodeficiency virus (HIV), herpes virus, adenovirus,
XX parvovirus, parvovirus, reovirus, orbivirus, picornavirus, rotavirus,
XX alphavirus, rubivirus, influenza virus (type A and type B), flavivirus,
XX coronavirus, paramyxovirus, morbillivirus, pneumovirus, rhabdovirus,

CC lyssavirus, orthomyxovirus, bunyavirus, phlebovirus, hantavirus,
CC hepadnavirus, arenavirus, retrovirus, enterovirus, rhinovirus, filovirus,
CC haemorrhagic fever virus, Chikungunya virus, Japanese encephalitis virus,
CC monkey pox virus, varicella virus, Congo-Crimean haemorrhagic fever virus,
CC Junin virus, Onkni haemorrhagic fever virus, Venezuelan equine
CC encephalitis virus, Dengue fever virus, Lassa fever virus, Rift valley
CC fever virus, western equine encephalitis virus, eastern equine
CC encephalitis virus, lymphocytic choriomeningitis virus, Russian spring-
CC summer encephalitis virus, white pox virus, Ebola virus, Machupo virus,
CC smallpox virus, yellow fever virus, Hantaan virus, Marburg virus or tick-
CC borne encephalitis virus. The present sequence represents a cyclic
CC antiviral peptide used in an example of the invention.

XX
SQ Sequence 8 AA;

Query Match 34.7%; Score 25; DB 8; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.1e+06;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 7 KSVKSLYL 14
|||
1 KSKKLYL 8

Db 1 KSKKLYL 8

RESULT 78
ADP67919
ID ADP67919 standard; peptide; 8 AA.
XX
AC ADP67919;
XX
DT 12-AUG-2004 (first entry)
XX
DE Anti-microbial cyclic peptide #83.
XX
KW microbial infection; cyclic; circular; anthrax infection;
KW staph infection; typhus; food poisoning; bacillary dysentery; pneumonia;
KW cholera; ulcer; botulism; smallpox; listeriosis; tularemia; plague;
KW bubonic plague; pneumonic plague; diarrhoea; hemorrhagic colitis;
KW haemolytic uremic syndrome; thrombotic thrombocytopenic purpura;
KW rabbit fever; deerfly fever; O'hara's disease.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 2 /note= "D-form residue"
FT Misc-difference 4 /note= "D-form residue"
FT Misc-difference 6 /note= "D-form residue"
FT Misc-difference 8 /note= "D-form residue"
FT Misc-difference 8 /note= "D-form residue"
XX
PN WO2003093300-A2.
XX
PD 13-NOV-2003.
XX
PF 06-MAY-2003; 2003WO-US014240.
XX
PR 06-MAY-2002; 2002WO-US014329.
XX
PI (SCRI) SCRIPPS RES INST.
XX
PI Ghadiri MR, Kim HS, Fernandez-Lopez S, Wilcoxen K;
XX
DR WPI; 2004-169024/16.
XX
PT Composition useful for the treatment of microbial infections e.g. anthrax
PT infection, staph infection comprises a cyclic peptide.
XX
PS Example 2; SEQ ID NO 83; 247pp; English.
XX
CC The invention comprises a composition for treating or preventing

CC microbial infection in an animal. The composition of the invention
CC contains a carrier and a cyclic peptide having a sequence of about 4-16
CC alternating D- and L-alpha-amino acids. The composition of the invention
CC is useful for the treatment of microbial infection, such as: anthrax
CC infection, staph infection, typhus, food poisoning, bacillary dysentery,
CC pneumonia, cholera, ulcers, botulism, smallpox, listeriosis, tularemia,
CC plague, bubonic plague, pneumonic plague, diarrhoea, hemorrhagic colitis,
CC haemolytic uremic syndrome, thrombotic thrombocytopenic purpura, rabbit
CC fever, deerfly fever and O'hara's disease. The present amino acid
CC sequence represents an anti-microbial cyclic peptide of the invention.

XX
SQ Sequence 8 AA;

Query Match 34.7%; Score 25; DB 8; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.1e+06;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 7 KSVKSLYL 14
|||
1 KSKKLYL 8

Db 1 KSKKLYL 8

RESULT 79
ADQ28132
ID ADQ28132 standard; peptide; 8 AA.
XX
AC ADQ28132;
XX
DT 09-SEP-2004 (first entry)
XX
DE Excluded cyclic antifungal peptide therapeutic agent #89.
XX
KW cyclic; fungicide; dermatological; antifungal; respiratory;
KW gastrointestinal; cardiovascular; uropathic; central nervous system;
KW auditory; fungal cell death inducer; medicament; fungal infection; human;
KW farm animal; systemic infection; topical infection;
KW dermatophytic fungal infection; onychomycosis; Epidermophyton;
KW Microsporium; Trichophyton rubrum; allergy; respiratory tract infection;
KW mucosal membrane infection; gastrointestinal tract infection;
KW cardiovascular infection; urinary tract infection; candidiasis;
KW mucocandidiasis; ringworm; tinea infection; athlete's foot; paronychia;
KW pityriasis versicolor; erythrasma; intertrigo; fungal nappy rash;
KW candida vulvitis; candida balanitis; otitis externa; cancer therapy;
KW transplant patient.
XX
OS Synthetic.
XX
PN WO2004050685-A2.
XX
PD 17-JUN-2004.
XX
PF 26-NOV-2003; 2003WO-US038595.
XX
PR 29-NOV-2002; 2002US-0429923P.
XX
PA (ADAP-) ADAPTIVE THERAPEUTICS INC.
PA (WEIN/) WEINBERGER D.
PA (SANC/) SANCHEZ-QUESADA J.
PA (CABE/) CABEZAS E.
XX
PI Sanchez-Quesada J, Cabezas E;
XX
DR WPI; 2004-487528/46.
XX
PT New peptide comprising a cyclic amino acid sequence of four to ten
PT alternating D- and L-alpha amino acids useful for treating fungal
PT infections.
XX
PS Claim 20; Page 66; 76pp; English.
XX
CC The invention relates to a peptide comprising a cyclic amino acid
CC sequence of 4-10 (preferably 6 or 8) alternating D- and L-alpha amino
CC acids (preferably polar, nonpolar and ionizable). The peptide is useful

CC in the manufacture of a medicament for treating or preventing fungal
 CC infection in an animal e.g. human, farm animal or companion animal
 CC including systemic, topical, dermatophytic fungal infection; for treating
 CC onychomycosis caused by Epidermophyton, Microsporum and Trichophyton
 CC rubrum; for treating allergy, respiratory tract infection, mucosal
 CC membrane infection, gastrointestinal tract infection, cardiovascular
 CC infection, urinary tract infection, CNS infection, candidiasis and
 CC chronic mucocandidiasis and skin infections caused by fungi, ringworm and
 CC trinea infections, athlete's foot, paronychia, pityriasis versicolor,
 CC erythrasma, intertrigo, fungal nappy rash, candida vulvitis, candida
 CC balanitis and ocular infections in immunocompromised patients
 CC (e.g. AIDS patients, patients receiving cancer therapy or transplant
 CC patients). The peptides possess antifungal activity without undesired
 CC anti-animal cell activity; have a minimum inhibitory concentration at
 CC which no target fungal organism grow in vitro is less than one twentieth
 CC to less than one half of the peptide concentration needed to cause 50%
 CC hemolysis of mammalian red blood cells in vitro ; causes no hemolysis of
 CC mammalian red blood cells in vitro ; are proteolytically stable and easy
 CC to synthesize and are highly effective against broad range of fungal
 CC infections. Sequences ADQ28003 to ADQ28043 correspond to claimed examples
 CC of the peptide of the invention. Specifically excluded as peptides of the
 CC invention are the sequences ADQ28044 to ADQ28180.

XX SQ Sequence 8 AA;

Query Match 34.7%; Score 25; DB 8; Length 8;

Best Local Similarity 75.0%; Pred. No. 2.1e+06; Mismatches 0; Gaps 0;

Matches 6; Conservative 0; Indels 2; Indels 0;

QY 7 KSVKSLYL 14

Db 1 KSSKYL 8

RESULT 80

ID AAR84828 standard; peptide; 9 AA.

XX AAR84828;

AC 25-APR-1996 (first entry)

XX Modified melanocyte-melanoma specific antigenic peptide G9-209-213W.

XX MART-1; M9-2; melanoma antigen recognised by T-cells; melanoma;

KM metastatic melanoma; tumour-associated antigen; immunogenic peptide;

KW diagnosis; prognosis; prophylaxis; therapy; vaccine.

XX Synthetic.

OS W09529193-A2.

XX 02-NOV-1995.

XX 21-APR-1995; 95WO-US005063.

XX 22-APR-1994; 94US-00231565.

PR 05-APR-1995; 95US-00417174.

XX (USSH) US SEC DEPT HEALTH.

XX Kawakami Y, Rosenberg SA;

XX WPI; 1995-382963/49.

XX DNA encoding melanoma antigens recognised by T-lymphocytes - also

PT vectors, host cells and antibodies, used to detect, treat and immunise

XX animal against melanoma.

XX Example 5; Page 107; 184pp; English.

XX AAR84816-836 are G9-209 peptides modified to improve immunogenicity. G9-

CC 209 is an immunogenic peptide based on the melanoma derived antigen,

CC gp100 (see AAR84210). The peptides are used in medicaments for the
 CC treatment or prevention (by immunization) of melanoma. Antibodies against
 CC MART-1 and its immunogenic peptides may be used in the detection and
 CC isolation of MART-1 from a sample, the detection of which is indicative
 CC of a disease state (melanoma or metastatic melanoma)

XX SQ Sequence 9 AA;

Query Match 34.7%; Score 25; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.1e+06; Mismatches 0; Gaps 0;

Matches 5; Conservative 0; Indels 0; Indels 0;

QY 1 VPFSV 5

Db 5 VPFSV 9

Search completed: July 12, 2006, 05:34:18

Job time : 218 secs

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103 15 20.8 13 2 S47382 T-cell antigen rec
 104 15 20.8 13 2 S47389 T-cell antigen rec
 105 15 20.8 13 2 PH0787 T-cell receptor al
 106 15 20.8 13 2 PC1008 40K extracellular
 107 15 20.8 13 2 S78766 ribosomal protein
 108 15 20.8 13 2 S74130 NADH oxidase - Gla
 109 15 20.8 14 2 A47421 leuotriene B-4 12
 110 15 20.8 14 2 JN0389 histamine-releasin
 111 15 20.8 14 2 PH1705 Ig heavy chain V r
 112 15 20.8 14 2 B34135 Ig heavy chain V r
 113 15 20.8 14 2 PH1566 DNA-binding protei
 114 15 20.8 14 2 A28018 cerebri 30 huma
 115 15 20.8 14 2 D35141 very late antigen
 116 15 20.8 14 2 C35141 T-cell receptor de
 117 15 20.8 14 2 E35141 T-cell receptor de
 118 15 20.8 14 2 B44854 T-cell receptor de
 119 15 20.8 15 2 S61284 L-2, 4-diaminobuty
 120 15 20.8 15 2 PS0452 phosphoprotein, 80
 121 15 20.8 15 2 PA0057 32K protein 3306 -
 122 15 20.8 15 2 PS0221 adenylate isopente
 123 15 20.8 15 2 S47387 gastrin-releasing
 124 15 20.8 15 2 PH1590 T-cell antigen rec
 125 15 20.8 15 2 B35141 Ig H chain V-D-J r
 126 15 20.8 15 2 A35141 T-cell receptor de
 127 15 20.8 15 2 PQ0781 NADH2 dehydrogenas
 128 15 20.8 15 2 S36896 ribosomal protein
 129 15 20.8 15 2 PA0053 protein QP200006 -
 130 15 20.8 15 2 A32921 beaded-chain filam
 131 15 20.8 15 2 PN0118 hemoglobin beta ch
 132 15 20.8 15 2 A54397 ubiquitin-carrier
 133 15 20.1 12 2 A54315 entactin/nidogen -
 134 14.5 20.1 15 2 PA0110 translatin elonga
 135 14 19.4 8 2 A61496 ubiquitin - celerly
 136 14 19.4 8 2 S37141 rpsa protein - Erw
 137 14 19.4 8 2 D47393 neurotrophin calla
 138 14 19.4 9 2 S70334 endosperm protein,
 139 14 19.4 9 2 S39766 cardioscactive pepi
 140 14 19.4 9 2 PT0285 Ig heavy chain CRD
 141 14 19.4 9 2 S77984 cytochrome-c oxida
 142 14 19.4 9 4 I73804 hypochetical E2 pr
 143 14 19.4 10 2 S39374 mannose receptor -
 144 14 19.4 10 2 PH1633 Ig H chain V-D-J r
 145 14 19.4 10 2 S06964 hypochetical prote
 146 14 19.4 10 2 D46285 formaldehyde dehyd
 147 14 19.4 10 2 G60787 sperm-activating p
 148 14 19.4 10 2 E60787 sperm-activating p
 149 14 19.4 11 2 PT0250 Ig heavy chain CRD
 150 14 19.4 11 2 PD0442 NIPSNAR2 protein
 151 14 19.4 11 2 S60294 tubulin 2 beta-3 c
 152 14 19.4 11 2 S78765 ribosomal protein
 153 14 19.4 11 2 B26744 megascoliakitin -
 154 14 19.4 12 2 S17869 glutathione transf
 155 14 19.4 12 2 PD0021 muconate cycloisom
 156 14 19.4 12 2 S10624 lipovitelin - Afr
 157 14 19.4 12 2 S65136 kalikrein K2 - hu
 158 14 19.4 12 2 S57570 T cell receptor V-
 159 14 19.4 12 2 PH0930 T-cell receptor be
 160 14 19.4 12 2 PH1470 T-cell receptor be
 161 14 19.4 12 2 S29859 gene p10 protein -
 162 14 19.4 12 2 PD00730 unidentified 5.4/3
 163 14 19.4 12 2 A56878 light yellow cell
 164 14 19.4 12 2 S56878 estrogen receptor
 165 14 19.4 12 2 I77529 NADH2 dehydrogenas
 166 14 19.4 13 2 S36887 ribosomal protein
 167 14 19.4 13 2 PS0325 tetrahydroberberin
 168 14 19.4 13 2 A54326 glandular kallikre
 169 14 19.4 13 2 PT0290 Ig heavy chain CRD
 170 14 19.4 13 2 S47377 T-cell antigen rec
 171 14 19.4 13 2 S47381 T-cell antigen rec
 172 14 19.4 13 2 S47385 T-cell antigen rec
 173 14 19.4 13 2 B36042 oxif protein - Bsc
 174 14 19.4 13 2 PN0168 phosphopyruvate hy
 175 14 19.4 14 1 QMVMHM mastoparan W - hor

176 14 19.4 14 1 QMVMHX mastoparan X - hor
 177 14 19.4 14 1 OMNAVY mastoparan - yello
 178 14 19.4 14 2 S19803 ubiquitin - potato
 179 14 19.4 14 2 I51432 histone H4-1 precu
 180 14 19.4 14 2 PT0077 proteochondotin c
 181 14 19.4 14 2 E61308 hemocyanin chain 3
 182 14 19.4 14 2 B20872 alpha-2-macroglobu
 183 14 19.4 14 2 S57574 T cell receptor V-
 184 14 19.4 14 2 PH0804 T-cell receptor al
 185 14 19.4 14 2 A54370 inorganic diphosph
 186 14 19.4 14 2 S58862 botulinum neurotox
 187 14 19.4 14 2 PQ0058 glycerol kinase (E
 188 14 19.4 14 2 S33802 chaperone, TCP1-re
 189 14 19.4 14 2 S14336 mastoparan B - hor
 190 14 19.4 14 2 PL0040 glycogen phosphory
 191 14 19.4 14 2 PC7075 guanylate cyclase
 192 14 19.4 14 2 E81280 probable proteolys
 193 14 19.4 15 2 PA0040 malate dehydrogena
 194 14 19.4 15 2 PS0276 phosphoribulokinas
 195 14 19.4 15 2 E41383 23K variable histo
 196 14 19.4 15 2 PA0026 protein QA300027 -
 197 14 19.4 15 2 PS0218 24K protein 4413 -
 198 14 19.4 15 2 B61457 alpha-glucosidase
 199 14 19.4 15 2 S57577 T cell receptor V-
 200 14 19.4 15 2 D46743 corneal keratan su
 201 14 19.4 15 2 S21293 RIP protein - rat
 202 14 19.4 15 2 PL0110 complement factor
 203 14 19.4 15 2 PT0095 H+-transporting tw
 204 14 19.4 15 2 PH1449 T-cell receptor al
 205 14 19.4 15 2 E91061 hypochetical prote
 206 14 19.4 15 2 S71920 proteinase ECP 32
 207 14 19.4 15 2 S36891 ribosomal protein
 208 14 19.4 15 2 S20410 protein kinase (EC
 209 14 19.4 15 2 PA0091 methionine adenosy
 210 14 19.4 15 2 PA0063 ubiquitin - fungus
 211 14 19.4 15 2 A60221 apolipoprotein A-I
 212 14 19.4 15 2 A61522 7.5K surfactant-as
 213 14 19.4 15 2 A32971 heparin-binding le
 214 14 19.4 15 2 S03955 acidic fibroblast
 215 14 19.4 15 2 PU0025 ubiquinol-cytochro
 216 14 19.4 15 2 I40665 iL1BN leader pepi
 217 13 18.1 15 2 PT0278 Ig heavy chain CRD
 218 13 18.1 15 2 PT0597 T-cell receptor be
 219 13 18.1 5 2 JS0319 subscophageal gang
 220 13 18.1 6 2 A61049 halo-toxin - pseud
 221 13 18.1 6 2 I51317 bHLH transcription
 222 13 18.1 7 2 PQ0663 membrane protein -
 223 13 18.1 7 2 PS0254 18K protein 5507 -
 224 13 18.1 7 2 E33932 Ig mu chain D regi
 225 13 18.1 7 2 A28340 myomodulin - Calif
 226 13 18.1 8 2 A42057 fibroblast growth
 227 13 18.1 8 2 A61467 penalbunin - Adeli
 228 13 18.1 8 2 I48934 apolipoprotein A-I
 229 13 18.1 8 2 T13818 cytochrome oxidase
 230 13 18.1 9 1 YEPG thymic factor - pi
 231 13 18.1 9 2 A60957 endosome growth p
 232 13 18.1 9 2 S70332 bradykinin - horn
 233 13 18.1 9 2 S65433 cardioscactive pepi
 234 13 18.1 9 2 S39767 cardioscactive pepi
 235 13 18.1 9 2 A26363 locustemycotropin I
 236 13 18.1 9 2 A61620 cardioscactive pepi
 237 13 18.1 9 2 S27233 serum amyloid P-co
 238 13 18.1 9 2 B20569 cyokeratin 4 - bo
 239 13 18.1 9 2 I46016 bone gla protein -
 240 13 18.1 9 2 I49406 hydroxyproline-3-b
 241 13 18.1 9 2 A43065 pev-tachykinin - p
 242 13 18.1 9 2 PU0027 vitamin D3 26-mono
 243 13 18.1 9 2 S15850 bradykinin-like pe
 244 13 18.1 9 2 A26744 Thr-6 bradykinin -
 245 13 18.1 9 2 A6057 bradykinin-like pe
 246 13 18.1 9 2 A60579 bradykinin - commo
 247 13 18.1 9 2 A61363 bradykinin-like pe
 248 13 18.1 9 2 A61358

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 T-cell receptor al
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 botulinum neurotox
 glycerol kinase (E
 chaperone, TCP1-re
 mastoparan B - hor
 glycogen phosphory
 guanylate cyclase
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 malate dehydrogena
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 23K variable histo
 protein QA300027 -
 24K protein 4413 -
 alpha-glucosidase
 T cell receptor V-
 corneal keratan su
 RIP protein - rat
 complement factor
 H+-transporting tw
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 hypochetical prote
 proteinase ECP 32
 ribosomal protein
 protein kinase (EC
 methionine adenosy
 ubiquitin - fungus
 apolipoprotein A-I
 7.5K surfactant-as
 heparin-binding le
 acidic fibroblast
 ubiquinol-cytochro
 iL1BN leader pepi
 Ig heavy chain CRD
 T-cell receptor be
 subscophageal gang
 halo-toxin - pseud
 bHLH transcription
 membrane protein -
 18K protein 5507 -
 Ig mu chain D regi
 myomodulin - Calif
 fibroblast growth
 penalbunin - Adeli
 apolipoprotein A-I
 cytochrome oxidase
 thymic factor - pi
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 cardioscactive pepi
 serum amyloid P-co
 cyokeratin 4 - bo
 bone gla protein -
 hydroxyproline-3-b
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 vitamin D3 26-mono
 bradykinin-like pe
 Thr-6 bradykinin -
 bradykinin-like pe
 bradykinin - commo
 bradykinin-like pe

249	13	18.1	10	2	PA0050	protein QA10052 -	322	13	18.1	14	2	PH1763	T cell receptor al
250	13	18.1	10	2	PS0209	24K protein 4407 -	322	13	18.1	14	2	S57569	T cell receptor V-
251	13	18.1	10	2	S65432	angiotensin I - ho	324	13	18.1	14	2	S57568	T cell receptor V-
252	13	18.1	10	2	A32195	Na+/K+-exchanging	325	13	18.1	14	2	PH1598	Ig H chain V-D-J r
253	13	18.1	10	2	A27617	triose-phosphate i	326	13	18.1	14	2	PH0765	T-cell receptor be
254	13	18.1	10	2	S77980	cytochrome-c oxida	327	13	18.1	14	2	PH0755	T-cell receptor be
255	13	18.1	10	2	A90345	angiotensin precu	328	13	18.1	14	2	PH1471	T-cell receptor be
256	13	18.1	10	2	C54226	light-harvesting p	329	13	18.1	14	2	B61597	cytochrome P450 AL
257	13	18.1	10	2	PO0788	NMDH2 dehydrogen	330	13	18.1	14	2	S21747	glutamate dehydrog
258	13	18.1	10	2	C60527	sperm-activating p	331	13	18.1	15	2	S24159	leukocyte elastase
259	13	18.1	11	2	A38841	rhodopsin homolog	332	13	18.1	15	2	A60834	angiotensin I prec
260	13	18.1	11	2	I54193	Rhesus blood group	333	13	18.1	15	2	I58116	Dp116 - human
261	13	18.1	11	2	PA0028	protein QA30042 -	334	13	18.1	15	2	S65717	prostaglandin D-sy
262	13	18.1	11	2	G61497	seed protein ws-23	335	13	18.1	15	2	PM0004	nitrogenase cofact
263	13	18.1	11	2	F31098	214K exantigen (v	336	13	18.1	15	2	S32577	hypothetical 1.7K
264	13	18.1	11	2	A54348	N-acetylglycosamin	337	13	18.1	15	2	UN0730	hypothetical 1.7K
265	13	18.1	11	2	PH1376	T antigen variant	338	13	18.1	15	2	PA0001	photosystem I iron
266	13	18.1	11	2	PH0938	T-cell receptor be	339	13	18.1	15	2	PA0024	photosystem I, iro
267	13	18.1	11	2	F58501	43.5K bile stone p	340	13	18.1	15	2	PA0114	photosystem I, iro
268	13	18.1	11	2	S66606	quinoline 2-oxidor	341	13	18.1	15	2	PA0080	translation elonga
269	13	18.1	11	2	S04875	nifs protein - Bra	342	13	18.1	15	2	S71300	ICL3 protein - Par
270	13	18.1	11	2	S69349	neuropeptide Frami	343	13	18.1	15	2	C61511	milk band B protei
271	13	18.1	11	2	S13279	lie-ser-bradykinin	344	13	18.1	15	2	PH1365	Ig heavy chain DJ
272	13	18.1	11	2	A59146	conotoxin ausa - c	345	13	18.1	15	2	S05700	insulin-like growt
273	13	18.1	11	2	S07207	Crina-angiotensin	346	13	18.1	15	2	D28587	T-cell receptor be
274	13	18.1	12	2	PN0581	tyrosine 3-monoxy	347	13	18.1	15	2	F28587	T-cell receptor be
275	13	18.1	12	2	PN0580	tyrosine 3-monoxy	348	13	18.1	15	2	PN0562	dystrophin-associ
276	13	18.1	12	2	PN0579	tyrosine 3-monoxy	349	13	18.1	15	2	I53284	T-cell receptor be
277	13	18.1	12	2	PN0577	tyrosine 3-monoxy	350	13	18.1	15	2	PD0444	coupling factor 6
278	13	18.1	12	2	PN0576	tyrosine 3-monoxy	351	13	18.1	15	2	I78838	flit3 ligand isofor
279	13	18.1	12	2	PN0578	tyrosine 3-monoxy	352	13	18.1	15	2	PT0097	glutathione peroxi
280	13	18.1	12	2	S26557	T-cell receptor be	353	13	18.1	15	2	PH0789	T-cell receptor al
281	13	18.1	12	2	S26556	T-cell receptor be	354	13	18.1	15	2	PH0770	T-cell receptor be
282	13	18.1	12	2	S26558	T-cell receptor be	355	13	18.1	15	2	PH0764	T-cell receptor be
283	13	18.1	12	2	S26554	T-cell receptor be	356	13	18.1	15	2	PH1436	capaid protein VPI
284	13	18.1	12	2	S26555	T-cell receptor be	357	13	18.1	15	2	PQ0545	carbon-monoxide de
285	13	18.1	12	2	S36899	ribosomal protein	358	13	18.1	15	2	PL0143	GMP-binding protei
286	13	18.1	12	2	PA0019	acidic ribosomal P	359	13	18.1	15	2	T03000	ribonucleoside-dip
287	13	18.1	12	2	S67528	napin - rape (frag	360	13	18.1	15	2	A17340	ribosomal protein
288	13	18.1	12	2	S18722	matk protein - bee	361	13	18.1	15	2	S36889	GLYMI - soybean
289	13	18.1	12	2	PH0746	T-cell receptor be	362	13	18.1	15	2	A56970	casein kinase II (
290	13	18.1	12	2	PH0771	T-cell receptor be	363	13	18.1	15	2	B45133	transforming prote
291	13	18.1	12	2	A49261	coagulation factor	364	13	18.1	15	2	C34874	acid phosphatase (
292	13	18.1	12	2	S65409	histone H2B - huma	365	13	18.1	15	2	A56963	pyrogallol hydroxy
293	13	18.1	13	2	PQ0491	self-incompatibili	366	13	18.1	15	2	S65429	avenin gamma-4 - c
294	13	18.1	13	2	E39778	lactase phosphotra	367	13	18.1	15	2	S29207	neuropeptide Led-c
295	13	18.1	13	2	B44957	protein L7 - commo	368	13	18.1	8	2	A44960	hypertrehalosemic
296	13	18.1	13	2	S09395	hypothetical prote	369	13	18.1	8	2	S08895	adipokinetic hormo
297	13	18.1	13	2	PT0331	Ig heavy chain CRD	370	13	18.1	8	2	A49823	adipokinetic hormo
298	13	18.1	13	2	D61458	Ig kappa chain V-I	371	13	18.1	8	2	A28804	nitrate reductase
299	13	18.1	13	2	B61458	Ig kappa chain V-I	372	13	18.1	8	2	S68802	205K exantigen -
300	13	18.1	13	2	G61458	Ig lambda chain V-	373	13	18.1	8	2	G33098	hypertrehalosemic
301	13	18.1	13	2	S47357	T-cell antigen rec	374	13	18.1	8	2	A39692	hypertrehalosemic
302	13	18.1	13	2	B47415	mannose-1-phosphat	375	13	18.1	8	2	S45651	R-phycocyanin ga
303	13	18.1	13	2	PH1593	Ig H chain V-D-J r	376	13	18.1	8	2	A37521	neuropeptide M-I -
304	13	18.1	13	2	PH1479	T-cell receptor be	377	13	18.1	8	2	A05169	apolipoprotein A-I
305	13	18.1	13	2	D56661	S-lucos specific g	378	13	18.1	8	2	I48935	phyllinocerulein -
306	13	18.1	13	2	S60046	early nodulin 40 -	379	13	18.1	9	2	A61357	fibronopeptide B -
307	13	18.1	13	2	S32474	lymadFamide 4 - g	380	13	18.1	9	2	D28854	macrophage chemota
308	13	18.1	13	2	S32475	lymadFamide 5 - g	381	13	18.1	10	2	A37027	6-phosphofructo-2-
309	13	18.1	13	2	B19434	probable sex-speci	382	13	18.1	10	2	A43405	hypertrehalosemic
310	13	18.1	13	2	PC4391	cysteine proteinas	383	13	18.1	10	2	S08997	hypertrehalosemic
311	13	18.1	13	2	G83988	hypothetical prote	384	13	18.1	10	2	A60421	hypertrehalosemic
312	13	18.1	13	2	S66558	serine proteinase	385	13	18.1	10	2	S08998	hypertrehalosemic
313	13	18.1	13	2	S21152	cryptophyllin-rela	386	13	18.1	10	2	A26381	hypertrehalosemic
314	13	18.1	13	2	A61361	bradykinin-like pe	387	13	18.1	10	2	A61337	caerulein - frog (
315	13	18.1	14	1	LFECM	trp operon leader	388	13	18.1	10	2	PT0322	Ig heavy chain CRD
316	13	18.1	14	1	PC2373	probable IMP dehyd	389	13	18.1	10	2	E41946	T-cell receptor ga
317	13	18.1	14	2	S21247	H+-transporting tw	390	13	18.1	10	2	D28027	protein P7 - curle
318	13	18.1	14	2	A01250	angiotensin precu	391	13	18.1	10	2	S62880	polygalacturonase
319	13	18.1	14	2	A49018	myosin heavy chain	392	13	18.1	10	2	PN0165	triose-phosphate i
320	13	18.1	14	2	E90858	trp operon leader	393	13	18.1	10	2	S53789	neuropeptide Pec-H
321	13	18.1	14	2	B85761	trp operon leader	394	13	18.1	10	2	D60787	sperm-activating p

395	12	16.7	10	2	E39572	sperm-activating p	468	12	16.7	15	2	PL0109	complement factor
396	12	16.7	10	2	D60589	sperm-activating p	469	12	16.7	15	2	A56049	urinary tract ston
397	12	16.7	10	2	A60588	sperm-activating p	470	12	16.7	15	2	PH1455	T-cell receptor al
398	12	16.7	11	2	A29806	acidic proline-rich	471	12	16.7	15	2	PC3374	unidentified 22k p
399	12	16.7	11	2	PT0218	T-cell receptor be	472	12	16.7	15	2	PC3093	emulatin synthetas
400	12	16.7	11	2	C49037	Ter gamma V-J reql	473	12	16.7	15	2	PA0093	protein QF200021 -
401	12	16.7	11	2	S78422	ribosomal protein	474	12	16.7	15	2	PA0059	neuropeptide pep -
402	12	16.7	11	2	I52304	gene rSSTR4 protei	475	12	16.7	15	2	PA0106	protein QF200076 -
403	12	16.7	11	2	I41138	acetyl ornithine d	476	12	16.7	15	2	A30330	urinary tract ston
404	12	16.7	11	2	I77447	urinary protein -	477	12	16.7	15	2	G24417	interphotoreceptor
405	12	16.7	11	4	PC2124	aminotransferase c	478	12	16.7	15	2	PT0096	pyruvate dehydroge
406	12	16.7	11	4	I52708	ELAV-like neuronal	479	12	16.7	15	2	PQ0780	NADH2 dehydrogenas
407	12	16.7	12	2	C36201	1-aminocyclopropan	480	12	16.7	11	15.3	I54357	Schwanomnin - mous
408	12	16.7	12	2	PH1675	Ig heavy chain V r	481	11	15.3	4	2	PL0146	carbon-monoxide de
409	12	16.7	12	2	S25056	Ig heavy chain - m	482	11	15.3	4	2	PT0551	T-cell receptor be
410	12	16.7	12	2	S11298	hemagglutinin prec	483	11	15.3	5	1	HOB0HA	protocollin - Americ
411	12	16.7	12	2	A26093	microbial collagen	484	11	15.3	5	2	A44955	alkenal monooxygen
412	12	16.7	12	2	S74196	3-Hydroxy-3-methyl	485	11	15.3	5	2	B22565	R-phycoerythrin al
413	12	16.7	12	2	S68402	NAD(+)-glycohydrol	486	11	15.3	5	2	PQ0009	angiotensin-conver
414	12	16.7	12	2	PH1581	Ig H chain V-D-J r	487	11	15.3	5	2	A60521	glycogen phosphory
415	12	16.7	12	2	H41946	T-cell receptor ga	488	11	15.3	5	2	A60411	proctocollin - Atlant
416	12	16.7	12	2	PH1457	T-cell receptor be	489	11	15.3	6	2	S02617	alcohol dehydrogen
417	12	16.7	12	2	PH1459	T-cell receptor be	490	11	15.3	6	2	B44510	hypothetical prote
418	12	16.7	12	2	S07206	kassinin - Senegal	491	11	15.3	6	2	I37263	hypothetical prote
419	12	16.7	13	2	A60856	inhibin alpha chai	492	11	15.3	6	2	I65546	Y protein - human
420	12	16.7	13	2	PH1676	Ig heavy chain V r	493	11	15.3	6	2	I59142	MHC H2-L antigen -
421	12	16.7	13	2	S15755	actin 7 - soybean	494	11	15.3	6	2	A41946	platelet-derived g
422	12	16.7	13	2	S38736	lipid transfer pro	495	11	15.3	6	2	I49424	T-cell receptor ga
423	12	16.7	13	2	S28425	20K protein - rape	496	11	15.3	7	2	E61491	cytotoxic T-lympho
424	12	16.7	13	2	E60396	antigen 7H8/2 - ma	497	11	15.3	7	2	S70335	seed protein ws-5
425	12	16.7	13	2	A33660	osteoclast functio	498	11	15.3	7	2	S78024	endosperm protein,
426	12	16.7	13	2	PT0256	Ig heavy chain CRD	499	11	15.3	7	2	A11483	ribosomal protein
427	12	16.7	13	2	S47376	T-cell antigen rec	500	11	15.3	7	2	B33541	aspartate transam
428	12	16.7	13	2	S47383	T-cell antigen rec	501	11	15.3	7	2	PT0520	hypothetical prote
429	12	16.7	13	2	B56864	dipeptidyl-peptida	502	11	15.3	7	2	PT0586	T-cell receptor be
430	12	16.7	13	2	A40207	cell surface glyco	503	11	15.3	7	2	PT0581	T-cell receptor be
431	12	16.7	13	2	A61514	glutathione transf	504	11	15.3	8	2	S63493	disintegratory sulf
432	12	16.7	13	2	S09018	hemolytic protein	505	11	15.3	8	2	PT0311	Ig heavy chain CRD
433	12	16.7	13	2	H85575	hypothetical prote	506	11	15.3	8	2	PN0043	phosphatidylethano
434	12	16.7	14	2	C40944	hypothetical prote	507	11	15.3	8	2	PL0162	paramyosin - north
435	12	16.7	14	2	A60622	somostatin - spo	508	11	15.3	8	2	S66645	cardioacceleratory
436	12	16.7	14	2	PH1677	Ig heavy chain V r	509	11	15.3	8	2	A42689	major postsynaptic
437	12	16.7	14	2	S60353	amylophilinlucanase	510	11	15.3	8	2	A35180	neutral proteinase
438	12	16.7	14	2	S35267	acetyl-CoA carboxy	511	11	15.3	9	2	A93408	oxytocin - Austral
439	12	16.7	14	2	PH1769	T cell receptor al	512	11	15.3	9	2	A92774	oxytocin - spotted
440	12	16.7	14	2	PH1626	Ig H chain V-D-J r	513	11	15.3	9	2	A93147	oxytocin - flinback
441	12	16.7	14	2	PH0800	T-cell receptor al	514	11	15.3	9	2	A91465	oxytocin - hippo
442	12	16.7	14	2	C48394	major fat-globule	515	11	15.3	9	2	B90667	oxytocin - rabbit
443	12	16.7	14	2	B56819	PS I complex subun	516	11	15.3	9	2	E28854	fibritinopeptide B -
444	12	16.7	14	2	S33801	chaperone, TCP1-re	517	11	15.3	9	2	PT0268	Ig heavy chain CRD
445	12	16.7	14	2	PS0249	porin - rice (stra	518	11	15.3	9	2	PT0324	Ig heavy chain CRD
446	12	16.7	14	2	B60683	malate dehydrogena	519	11	15.3	9	2	B46250	alpha-adaptcin - bo
447	12	16.7	14	2	PC4376	telomeric and tetr	520	11	15.3	9	2	PH1591	Ig H chain V-D-J r
448	12	16.7	14	4	S29878	Na+/K+-exchangin	521	11	15.3	9	2	J01202	leader peptide - p
449	12	16.7	14	4	I52618	hemoglobin beta ch	522	11	15.3	10	1	XASNPC	angiotensin-conver
450	12	16.7	15	2	A47146	topoisomerase I -	523	11	15.3	10	2	S71868	glutathione transf
451	12	16.7	15	2	C37765	hypothetical prote	524	11	15.3	10	2	S66458	ferridoxin - Rhizo
452	12	16.7	15	2	PA0016	glycine cleavage T	525	11	15.3	10	2	S48182	bacterioferritin -
453	12	16.7	15	2	PA0046	protein OA100044 -	526	11	15.3	10	2	JP0072	ribosomal protein
454	12	16.7	15	2	PA0009	seed storage prote	527	11	15.3	10	2	PT0038	glutathione transf
455	12	16.7	15	2	PS0208	20K protein 5403 -	528	11	15.3	10	2	C61440	polygalacturonase
456	12	16.7	15	2	PA0052	protein QF200015 -	529	11	15.3	10	2	C39111	Ig heavy chain C r
457	12	16.7	15	2	PA0051	protein QF200016 -	530	11	15.3	10	2	PT0243	Ig heavy chain CRD
458	12	16.7	15	2	PT0222	Ig heavy chain CDR	531	11	15.3	10	2	PT0251	Ig heavy chain CRD
459	12	16.7	15	2	PH1366	Ig heavy chain DJ	532	11	15.3	10	2	S23371	T-cell receptor al
460	12	16.7	15	2	PH1318	Ig heavy chain DJ	533	11	15.3	10	2	I48778	small nuclear ribo
461	12	16.7	15	2	S55312	TSH protein beta c	534	11	15.3	10	2	PH0807	T-cell receptor al
462	12	16.7	15	2	A27504	histone H2A - mous	535	11	15.3	10	2	D54823	olfactory receptor
463	12	16.7	15	2	PH1616	Ig H chain V-D-J r	536	11	15.3	10	2	S65715	aryl hydrocarbon (
464	12	16.7	15	2	PH1619	Ig H chain V-D-J r	537	11	15.3	10	2	S65385	cytochrome-c oxida
465	12	16.7	15	2	PH0775	T-cell receptor al	538	11	15.3	10	2	C35389	urease (EC 3.5.1.5
466	12	16.7	15	2	PH0779	T-cell receptor al	539	11	15.3	10	2	A44646	neurotoxin-associa
467	12	16.7	15	2	A49887	transcription fact	540	11	15.3	10	2	I44644	neurotoxin-associa

541	11	15.3	10	2	S38305	614	11	15.3	13	2	PT0305	Ig heavy chain CRD
542	11	15.3	10	2	PX0030	615	11	15.3	13	2	S70441	pancreatic elastase
543	11	15.3	10	2	B61440	616	11	15.3	13	2	S47378	T-cell antigen rec
544	11	15.3	10	2	S43630	617	11	15.3	13	2	S23372	T-cell receptor al
545	11	15.3	10	2	S43631	618	11	15.3	13	2	S10562	zona pellucida-bin
546	11	15.3	10	2	A30823	619	11	15.3	13	2	B25448	Ig kappa-1 chain,
547	11	15.3	10	2	F33932	620	11	15.3	13	2	A32486	beta protein - rat
548	11	15.3	10	2	C54823	621	11	15.3	13	2	D47630	Ig kappa chain J r
549	11	15.3	10	2	A61318	622	11	15.3	13	2	S03063	Ig lambda chain J
550	11	15.3	10	2	B61318	623	11	15.3	13	2	A59387	VCAM-1 5'UTR bindi
551	11	15.3	10	2	T13838	624	11	15.3	13	2	A32453	phloroglucinol red
552	11	15.3	10	2	T12312	625	11	15.3	13	2	G22565	R-phycocerythrin ga
553	11	15.3	10	2	PQ0785	626	11	15.3	13	2	S14316	photosystem I 9K c
554	11	15.3	10	2	PQ0783	627	11	15.3	13	2	S09733	photosystem I prot
555	11	15.3	10	2	C60787	628	11	15.3	13	2	D61491	seed protein I
556	11	15.3	10	2	C60588	629	11	15.3	13	2	PQ0700	unidentified 6.3/4
557	11	15.3	10	2	E60527	630	11	15.3	13	2	G56046	urinary tract ston
558	11	15.3	10	2	S07202	631	11	15.3	13	2	S32551	glutathione transf
559	11	15.3	10	2	C61033	632	11	15.3	14	2	S22236	lipoxigenase (EC 1
560	11	15.3	10	2	B61033	633	11	15.3	14	2	S62374	alpha-1-antichymot
561	11	15.3	10	2	S27178	634	11	15.3	14	2	PA0109	porin por 1B - Ara
562	11	15.3	10	2	C45474	635	11	15.3	14	2	B56863	photosystem I reac
563	11	15.3	11	1	ECLO2M	636	11	15.3	14	2	A61002	photosystem II oxy
564	11	15.3	11	1	PN0042	637	11	15.3	14	2	E33098	metal-binding prot
565	11	15.3	11	2	A40693	638	11	15.3	14	2	PL0152	DEB-A protein - fr
566	11	15.3	11	2	E60691	639	11	15.3	14	2	S38307	cell surface alloa
567	11	15.3	11	2	A34135	640	11	15.3	14	2	A60770	Ig heavy chain DJ
568	11	15.3	11	2	PT0301	641	11	15.3	14	2	PH1348	Ig heavy chain DJ
569	11	15.3	11	2	S68649	642	11	15.3	14	2	PH1322	Ig heavy chain DJ
570	11	15.3	11	2	S45386	643	11	15.3	14	2	PH1311	Ig heavy chain DJ
571	11	15.3	11	2	S35490	644	11	15.3	14	2	S47366	T-cell antigen rec
572	11	15.3	11	2	B39853	645	11	15.3	14	2	S23369	T-cell receptor al
573	11	15.3	11	2	A55149	646	11	15.3	14	2	PH0135	T-cell receptor be
574	11	15.3	11	2	S33519	647	11	15.3	14	2	B28018	very late antigen-
575	11	15.3	11	2	C61497	648	11	15.3	14	2	A43847	Ig mu chain V regl
576	11	15.3	11	2	S19775	649	11	15.3	14	2	JS0272	hypothetical 1.5K
577	11	15.3	11	2	PC4267	650	11	15.3	14	2	PH1614	Ig H chain V-D-J r
578	11	15.3	11	2	A26120	651	11	15.3	14	2	PH1617	Ig H chain V-D-J r
579	11	15.3	11	2	S21727	652	11	15.3	14	2	PH1623	Ig H chain V-D-J r
580	11	15.3	11	2	A14454	653	11	15.3	14	2	PH1608	Ig H chain V-D-J r
581	11	15.3	11	2	A34243	654	11	15.3	14	2	PH0792	T-cell receptor al
582	11	15.3	11	2	S23306	655	11	15.3	14	2	S29632	xylin 1,4-beta-xy
583	11	15.3	12	1	A43975	656	11	15.3	14	2	PA0045	porin por1 - Arabi
584	11	15.3	12	1	S11286	657	11	15.3	14	2	PN0147	omega-gliadin 1 a
585	11	15.3	12	2	I64829	658	11	15.3	14	2	PT0029	karatsasin - kara
586	11	15.3	12	2	S26559	659	11	15.3	14	2	S45655	cathepsin L (EC 3,
587	11	15.3	12	2	C39109	660	11	15.3	14	2	S00150	ovostatin - duck (
588	11	15.3	12	2	C64030	661	11	15.3	15	1	B36079	hypothetical prote
589	11	15.3	12	2	S49547	662	11	15.3	15	1	SFRP	scotophobin - rat
590	11	15.3	12	2	PH1324	663	11	15.3	15	2	NTKNAG	alpha-conotoxin GI
591	11	15.3	12	2	PH1308	664	11	15.3	15	2	PA0041	plasmaconol-plast
592	11	15.3	12	2	S47393	665	11	15.3	15	2	B61243	dimethylamline mo
593	11	15.3	12	2	S47394	666	11	15.3	15	2	S14749	3-dehydroquinase -
594	11	15.3	12	2	PH1183	667	11	15.3	15	2	PQ0195	Sfil-glycoprotein
595	11	15.3	12	2	S74144	668	11	15.3	15	2	S21240	alpha-glucosidase
596	11	15.3	12	2	PH1587	669	11	15.3	15	2	S21241	oligo-1,6-glucosid
597	11	15.3	12	2	S39762	670	11	15.3	15	2	PC2215	fibrinolytic p
598	11	15.3	12	2	PH0920	671	11	15.3	15	2	A22789	platelet-derived g
599	11	15.3	12	2	PH1467	672	11	15.3	15	2	A49185	vasotocin-associat
600	11	15.3	12	2	PH1458	673	11	15.3	15	2	PH1319	Ig heavy chain DJ
601	11	15.3	12	2	PH1466	674	11	15.3	15	2	S26527	T-cell receptor al
602	11	15.3	12	2	S71034	675	11	15.3	15	2	PS0382	Ig heavy chain J r
603	11	15.3	12	2	PA0047	676	11	15.3	15	2	B56661	S-locus specific g
604	11	15.3	12	2	PN0162	677	11	15.3	15	2	PA0034	protein Qa300024 -
605	11	15.3	12	2	PA0098	678	11	15.3	15	2	S29386	nigermycin - Desu
606	11	15.3	12	2	A61503	679	11	15.3	15	2	A56863	photosystem I reac
607	11	15.3	12	2	B32521	680	11	15.3	15	2	T46625	hypothetical prote
608	11	15.3	12	2	F84132	681	11	15.3	15	2	PA0014	seed storage prote
609	11	15.3	13	1	UNBO	682	11	15.3	15	2	PN0173	seed storage prote
610	11	15.3	13	1	UNOBT	683	11	15.3	15	2	S13973	chlorophyll a/b-bi
611	11	15.3	13	2	A53608	684	11	15.3	15	2	S08209	hypothetical prote
612	11	15.3	13	2	H44957	685	11	15.3	15	2	S62620	protein disulfide-
613	11	15.3	13	2	A23694	686	11	15.3	15	2	PQ0192	stylar glycoprotei

687 11 15.3 15 2 P00193 stylar glycoprotei
 688 11 15.3 15 2 PA0095 protein QF200056 -
 689 11 15.3 15 2 PN0144 serine proteinase
 690 11 15.3 15 2 S10386 Ig heavy chain J r
 691 11 15.3 15 2 S10386 Ig heavy chain J r
 692 11 15.3 15 2 B41436 ovostatin - green
 693 11 15.3 15 2 S60007 glial hyaluronate-
 694 11 15.3 15 2 PH1314 Ig heavy chain DJ
 695 11 15.3 15 2 PH1320 Ig heavy chain DJ
 696 11 15.3 15 2 PH1762 T cell receptor al
 697 11 15.3 15 2 PH1788 T cell receptor al
 698 11 15.3 15 2 S47367 T-cell antigen rec
 699 11 15.3 15 2 A49252 T-cell receptor be
 700 11 15.3 15 2 PH0136 T-cell receptor be
 701 11 15.3 15 2 B56046 urinary tract ston
 702 11 15.3 15 2 F44823 synaptosomal-assoc
 703 11 15.3 15 2 PH1610 Ig H chain V-D-J r
 704 11 15.3 15 2 PH1378 T antigen variant
 705 11 15.3 15 2 PH1377 T antigen variant
 706 11 15.3 15 2 PH0808 T-cell receptor al
 707 11 15.3 15 2 B26501 lipoprotein lipase
 708 11 15.3 15 2 S72431 epoxypropan isomer
 709 11 15.3 15 2 PH0091 H+-transporting tw
 710 11 15.3 15 2 PH00778 NADH2 dehydrogenas
 711 11 15.3 15 2 S61438 hypothetical prote
 712 11 15.3 15 2 PH0216 agatase (EC 3.2.1.
 713 11 15.3 15 2 A41338 isocitrate lyase (I
 714 11 15.3 15 2 A26228 spot 42 protein -
 715 11 15.3 15 2 C43334 orf3 3' to aadr -
 716 11 15.3 15 2 S03353 plactocyanin - Mic
 717 11 15.3 15 2 S36890 ribosomal protein
 718 11 15.3 15 2 A40634 orf19 3' of eryK -
 719 11 15.3 15 2 A48372 benzoyl-CoA ligase
 720 11 15.3 15 2 PA0036 glycine cleavage s
 721 11 15.3 15 2 PA0005 lectin A1 - psopio
 722 11 15.3 15 2 PA0006 lectin A3 - psopio
 723 11 15.3 15 2 PS0450 23k protein 4307 -
 724 11 15.3 15 2 PS0455 superoxide dismuta
 725 11 15.3 15 2 PA0105 heat shock protein
 726 11 15.3 15 2 PA0071 superoxide dismuta
 727 11 15.3 15 2 B49177 21k protein p2, mi
 728 11 15.3 15 2 A49177 22k protein p1, mi
 729 11 15.3 15 2 A36279 chemotactant pr
 730 11 15.3 15 2 PC1313 small granule S6 c
 731 11 15.3 15 2 A61612 allostatin - tob
 732 11 15.3 15 2 PT0090 alpha-glucosidase
 733 11 15.3 15 2 S77988 cytochrome-c oxida
 734 11 15.3 15 2 B45115 peptidylprolyl iso
 735 11 15.3 15 2 A35417 28k serine protein
 736 11 15.3 15 2 I46909 voltage-dependent
 737 11 15.3 15 2 PT0094 succinate dehydrog
 738 11 15.3 15 2 S04586 NADH2 dehydrogenas
 739 11 15.3 15 4 I38032 hypothetical MN1/T
 740 11 15.3 15 4 I38031 hypothetical MN1/T
 741 11 15.3 15 4 I38888 COI intron 16 prot
 742 10 13.9 4 2 PT0240 Ig heavy chain CRD
 743 10 13.9 4 2 A53284 T-cell receptor be
 744 10 13.9 4 2 PT0721 T-cell receptor be
 745 10 13.9 4 2 A32039 tyrosine-melanocyt
 746 10 13.9 5 2 B37325 pap fibribrial regul
 747 10 13.9 5 2 S11127 phosphoprotein, bo
 748 10 13.9 5 2 D44823 synaptosomal-assoc
 749 10 13.9 5 2 PT0625 T-cell receptor be
 750 10 13.9 5 2 PT0660 T-cell receptor be
 751 10 13.9 6 2 PT0713 T-cell receptor be
 752 10 13.9 6 2 A60494 antineoplastic gly
 753 10 13.9 6 2 H48394 glycoprotein compo
 754 10 13.9 6 2 B26206 alpha-1,4-glucan-p
 755 10 13.9 6 2 A20186 fatty-acid synthas
 756 10 13.9 6 2 PT0519 T-cell receptor be
 757 10 13.9 6 2 PT0643 T-cell receptor be
 758 10 13.9 6 2 PT0621 T-cell receptor be
 759 10 13.9 6 2 PT0560 T-cell receptor be

760 10 13.9 6 2 PT0718 T-cell receptor be
 761 10 13.9 6 2 PT0727 T-cell receptor be
 762 10 13.9 6 2 PT0730 T-cell receptor be
 763 10 13.9 6 2 PD0028 pev-kinin 2 - pena
 764 10 13.9 6 2 A61068 locustactinin - mig
 765 10 13.9 7 2 S55548 mecb protein - Esc
 766 10 13.9 7 2 S42407 gramicidin S synh
 767 10 13.9 7 2 A33098 244k exantigen -
 768 10 13.9 7 2 PT0246 Ig heavy chain CRD
 769 10 13.9 7 2 PH1602 Ig H chain V-D-J r
 770 10 13.9 7 2 PT0521 T-cell receptor be
 771 10 13.9 7 2 PT0663 T-cell receptor be
 772 10 13.9 7 2 PT0579 T-cell receptor be
 773 10 13.9 7 2 PD0029 pev-kinin 1 - pena
 774 10 13.9 7 2 S29735 polyphosphate-gluc
 775 10 13.9 7 2 T09512 NADH2 dehydrogenas
 776 10 13.9 7 2 PT0529 T-cell receptor be
 777 10 13.9 7 2 A61081 tryptophyllin, bas
 778 10 13.9 8 2 S11545 adipoiknetic hormo
 779 10 13.9 8 2 A61348 red pigment-concen
 780 10 13.9 8 2 A43976 hypertrehaosemic
 781 10 13.9 8 2 B43975 hypertrehaosemic
 782 10 13.9 8 2 T10952 hypothetical prote
 783 10 13.9 8 2 S13661 polygalacturonase
 784 10 13.9 8 2 PT0368 Ig gamma chain C r
 785 10 13.9 8 2 PT0323 Ig heavy chain CRD
 786 10 13.9 8 2 B45800 serum albumin - do
 787 10 13.9 8 2 PT0627 T-cell receptor be
 788 10 13.9 8 2 PT0559 T-cell receptor be
 789 10 13.9 8 2 PT0554 T-cell receptor be
 790 10 13.9 8 2 PT0716 T-cell receptor be
 791 10 13.9 8 2 PT0725 T-cell receptor be
 792 10 13.9 8 2 PC4372 telomeric and letr
 793 10 13.9 8 2 S65647 2-hydroxyglucaryl-
 794 10 13.9 8 2 PT0030 inlinase (EC 3.2.
 795 10 13.9 8 2 US0315 leucokinin V - Mad
 796 10 13.9 8 2 US0317 leucokinin VII - M
 797 10 13.9 8 2 E47393 neuropeptide calla
 798 10 13.9 8 2 A59028 MHC class I histoc
 799 10 13.9 8 4 I54017 granulocyte-colony
 800 10 13.9 9 2 A44873 caldesmon - rabbit

ALIGNMENTS

RESULT 1

PH0774 T-cell receptor beta chain (RF3.10.3) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999

C:Accession: PH0774
 R:Caanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
 J. Exp. Med. 174, 1371-1383, 1991

A>Title: T cell receptor genes in a series of class I major histocompatibility complex-r
 allelic exclusion and antigen-specific repertoire.
 A:Reference number: PH0746; MUID:92078846; PMID:1836010

A:Accession: PH0774
 A:Molecule type: mRNA
 A:Residues: 1-14 <CAS>

A:Cross-references: UNIPARC:UP10000115FC1; EMBL:X60870; NID:G53975; PIDN:CAA43258.1; PID
 A:Experimental source: T lymphocyte
 C:Keywords: T-cell receptor

Query Match 34.7%; Score 25; DB 2; Length 14;

Best Local Similarity 41.7%; Pred. No. 3.2e+02;

Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 4 SVAKSVKSLVNG 15

DB 3 SSSASAEFLVFG 14

RESULT 2

C59137

protein pf3 - golden needle mushroom (fragment)

C:Species: Flammulina velutipes (golden needle mushroom)

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: C59137

R:Sakamoto, Y.; Ando, A.; Tamai, Y.; Miura, K.

submitted to the Protein Sequence Database, November 1999

A:Description: Differences of proteins expressed in the fruiting dikaryon and the non-fr

A:Reference number: A59137

A:Accession: C59137

A:Molecule type: protein

A:Residues: 1-14 <SAKS>

A:Cross-references: UNIPROT:Q7M4M9; UNIPARC:UPI000017CB24

Query Match

34.7%; Score 25; DB 2; Length 14;

Best Local Similarity 66.7%; Pred. No. 3.2e+02;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPSVA 6

DB 9 VPSIS 14

RESULT 3

S49409

H+-transporting two-sector ATPase (EC 3.6.3.14) chain a - Streptococcus oralis (fragment

C:Species: Streptococcus oralis

C:Date: 29-Nov-1995 #sequence_revision 01-Aug-1997 #text_change 31-Dec-2004

C:Accession: S49409; S38211

R:Penoll, A.; Munoz, R.; Garcia, E.; de la Campa, A.G.

Mol. Microbiol. 12, 587-598, 1994

A:Title: Molecular basis of the optochin-sensitive phenotype of pneumococcus: characteri

ases.

A:Reference number: S49398; MID:95020593; PMID:7934862

A:Accession: S49409

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-15 <FEN>

A:Cross-references: UNIPROT:Q60249; UNIPARC:UPI0000170206; EMBL:Z26853; NID:9407180; PTD

C:Keywords: ATP biosynthesis; hydrolase; membrane-associated complex

Query Match

33.3%; Score 24; DB 2; Length 15;

Best Local Similarity 57.1%; Pred. No. 5.4e+02;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 9 VMSLYIG 15

DB 1 LSSMYIG 7

RESULT 4

A44871

monodehydroascorbate reductase (NADH2) (EC 1.6.5.4) - soybean (fragment)

C:Species: Glycine max (soybean)

C:Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C:Accession: A44871

R:Dalton, D.A.; Langeberg, L.; Robbins, M.

Arch. Biochem. Biophys. 292, 281-286, 1992

A:Title: Purification and characterization of monodehydroascorbate reductase from soybea

A:Reference number: A44871; MID:92088257; PMID:1727643

A:Accession: A44871

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-10 <DAL>

A:Cross-references: UNIPROT:Q9S926; UNIPARC:UPI000009DB60

A:Experimental source: root nodules, cv. Williams

A:Note: sequence extracted from NCBI backbone (NCBIP:17052)

C:Keywords: oxidoreductase

Query Match

31.9%; Score 23; DB 2; Length 10;

Best Local Similarity 50.0%; Pred. No. 5.4e+02;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 AKSVKSLYIG 15

DB 1 AKTFKXIIIG 10

RESULT 5

S47372

T-cell antigen receptor VJ junction beta chain - human

C:Species: Homo sapiens (man)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999

C:Accession: S47372

R:Lehner, P.U.

submitted to the EMBL Data Library, August 1994

A:Description: Human HLA-A*0201 restricted recognition of influenza A is dominated by T

A:Reference number: S47355

A:Accession: S47372

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-13 <LEH>

A:Cross-references: UNIPARC:UPI0000116684; EMBL:Z35697; NID:9527485; PTD:CAA84766.1; P

Query Match

31.9%; Score 23; DB 2; Length 13;

Best Local Similarity 50.0%; Pred. No. 7.1e+02;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 AKSVKSLY 13

DB 2 ASSIRSAV 9

RESULT 6

JN0390

histamine-releasing peptide II - oriental hornet

N:Alternate names: venom protein HR-2

C:Species: Vespa orientalis (oriental hornet)

C:Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 09-Jul-2004

C:Accession: JN0390; S10919

R:Miroschnikov, A.I.; Snezhkova, L.G.; Nazimov, I.V.; Reshetova, O.I.; Rozinov, B.V.; Gu

Bioorg. Khim. 7, 1467-1477, 1981

A:Title: Structure and properties of histamine releasing peptides from the venom of Vespa

A:Reference number: JN0389

A:Accession: JN0390

A:Molecule type: protein

A:Residues: 1-14 <MTR>

A:Cross-references: UNIPROT:P17236; UNIPARC:UPI0000035436

R:Tuchinbaev, M.U.; Akmedova, N.U.; Kazakov, I.; Korneev, A.S.; Gagel'gans, A.I.

Biochemistry (N.Y.) 53, 183-190, 1988

A:Title: Low-molecular-weight peptides of venom of the giant hornet Vespa orientalis. S

A:Reference number: S06445

A:Accession: S10919

A:Molecule type: protein

A:Residues: 1-14 <TUI>

A:Cross-references: UNIPARC:UPI0000035436

C:Superfamily: crabrolin

C:Keywords: amidated carboxyl end; venom

F:14/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match

31.9%; Score 23; DB 2; Length 14;

Best Local Similarity 41.7%; Pred. No. 7.7e+02;

Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 VPSVAKSVKSL 12

DB 2 LPLILGKLVKGL 13

RESULT 7

G61308

hemocyanin chain 3C - Sahara scorpion (fragment)

C:Species: Androctonus australis (Sahara scorpion)

C>Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 09-Jul-2004
C/Accession: G61308
C/Species: J.; Jolles, P.; Lamy, J.; Lamy, J.
C/Date: 106, 289-291, 1979
C/Title: Structural characterization of seven different subunits in Androctonus australis
C/Accession: A61308; MUID:80047238; PMID:499512
A/Reference number: G61308
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-14 <JOL>
A/Cross-references: UNIPROT:Q7M487; UNIPARC:UPI000017BE01

Query Match 31.9%; Score 23; DB 2; Length 14;
Best Local Similarity 25.0%; Pred. No. 7.7e+02;
Matches 3; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 PFSVAKSVKSLY 13
| : : : : |
DB 2 PNIQRITSLP 13

RESULT 8

S47365
T-cell antigen receptor VI junction beta chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C/Accession: S47365; S47375; S47379; S47396; S47397; S47398; S47355
R/Lehner, P.J.
Submitted to the EMBL Data Library, August 1994
A/Description: Human HLA-A*0201 restricted recognition of influenza A is dominated by T c
A/Reference number: S47355
A/Accession: S47365
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-13 <LEH>
A/Cross-references: UNIPARC:UPI0000116673; EMBL:Z35690; NID:G527471; PIDN:CAA84759.1; PI
A/Accession: S47375
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-13 <LE2>
A/Cross-references: UNIPARC:UPI0000116673; EMBL:Z35700; NID:G527493; PIDN:CAA84769.1; PI
A/Accession: S47379
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-13 <LE3>
A/Cross-references: UNIPARC:UPI0000116673; EMBL:Z35708; NID:G527509; PIDN:CAA84777.1; PI
A/Accession: S47396
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-13 <LE4>
A/Cross-references: UNIPARC:UPI0000116673; EMBL:Z35674; NID:G527527; PIDN:CAA84743.1; PI
A/Accession: S47397
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-13 <LE5>
A/Cross-references: UNIPARC:UPI0000116673; EMBL:Z35675; NID:G527529; PIDN:CAA84744.1; PI
A/Accession: S47398
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-13 <LE6>
A/Cross-references: UNIPARC:UPI0000116673; EMBL:Z35676; NID:G527531; PIDN:CAA84745.1; PI
C/Keywords: T-cell receptor

Query Match 30.6%; Score 22; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 AKSVKSLY 13
| : : : : |
DB 2 ASSIRSSY 9

RESULT 9

S43634

Cytochrome-c oxidase (EC 1.9.3.1) chain VIIC, cardiac - rainbow trout (fragment)
C/Species: Oncorhynchus mykiss (rainbow trout)
C/Date: 20-Oct-1994 #sequence_revision 01-Nov-1996 #text_change 16-Jul-1999
C/Accession: S43634
C/Reference number: S43634
C/Date: 221, 111-116, 1994
C/Title: Identification of tissue-specific isoforms for subunits Vb and VIIa of cytochrome
A/Reference number: S43624; MUID:94237150; PMID:8181469
A/Accession: S43634
A/Molecule type: protein
A/Residues: 1-15 <PRE>
A/Cross-references: UNIPARC:UPI000017BF5A
A/Note: the source is designated as Salmo gairdneri
C/Genetics:
A/Genome: nuclear

C/Keywords: cardiac muscle; heart; membrane-associated complex; mitochondrion; oxidoredu

Query Match 30.6%; Score 22; DB 2; Length 15;
Best Local Similarity 80.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFVS 5
| : : : : |
DB 11 LPFSV 15

RESULT 10

E45691
Probable minor capsid protein R117a [similarity] - Lactobacillus delbrueckii subsp. lact
C/Species: Lactobacillus delbrueckii subsp. lactis phage L1-H
C/Date: 24-Feb-1994 #sequence_revision 25-Apr-1997 #text_change 05-Oct-2004
C/Accession: E45691
R/Vasala, A.; Dupont, L.; Baumann, M.; Ritzenhaler, P.; Alcossega, T.
J. Virol. 67, 3061-3068, 1993
A/Title: Molecular comparison of the structural proteins encoding gene clusters of two r
A/Reference number: A45691; MUID:93267750; PMID:8497043
A/Accession: E45691
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-12 <VAS>
A/Cross-references: UNIPROT:O04769; UNIPARC:UPI000017986E
A/Note: sequence extracted from NCBI backbone (NCBIN:132363, NCBI:132373)
C/Superfamily: uncharacterized conserved protein

Query Match 27.8%; Score 20; DB 2; Length 12;
Best Local Similarity 37.5%; Pred. No. 2.4e+03;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 VPFVS 8
| : : : : |
DB 5 IPQWAVS 12

RESULT 11

S47360
T-cell antigen receptor VJ junction beta chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C/Accession: S47360
R/Lehner, P.J.
Submitted to the EMBL Data Library, August 1994
A/Description: Human HLA-A*0201 restricted recognition of influenza A is dominated by T c
A/Reference number: S47355
A/Accession: S47360
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-12 <LEH>
A/Cross-references: UNIPARC:UPI000011667A; EMBL:Z35684; NID:G527457; PIDN:CAA84753.1; PI
C/Keywords: T-cell receptor

Query Match 27.8%; Score 20; DB 2; Length 12;
Best Local Similarity 57.1%; Pred. No. 2.4e+03;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 AKSVKSL 12
| | | |
Db 6 AKSISL 12

RESULT 12

S47374
T-cell antigen receptor VJ junction beta chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 25-Oct-1996 #text_change 05-Nov-1999
C:Accession: S47374; S47399; S47364
R:Lehner, P.J.
Submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A*0201 restricted recognition of influenza A is dominated by T
A:Reference number: S47355
A:Accession: S47374
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: UNIPARC:UPI0000116674; EMBL:Z35699; NID:9527491; PIDN:CAA84768.1; PI
A:Accession: S47399
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEZ>
A:Cross-references: UNIPARC:UPI0000116674; EMBL:Z35677; NID:9527533; PIDN:CAA84746.1; PI
C:Keywords: T-cell receptor

Query Match 27.8%; Score 20; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 2.6e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 AKSVKSLY 13
| | | | |
Db 2 ASSMRSSY 9

RESULT 13

I70075
glycophorin B (mistranslated) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 21-Feb-1997 #sequence_revision 14-Aug-1997 #text_change 09-Jul-2004
C:Accession: I70075
R:Rearden, A.; Phan, H.; Dubnicoff, T.; Kudo, S.; Fukuda, M.
J. Biol. Chem. 265, 9259-9263, 1990
A:Title: Identification of the crossing-over point of a hybrid gene encoding human glyco
A:Reference number: I55334; MUID:90264417; PMID:1971625
A:Accession: I70075
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-13 <REA>
A:Cross-references: UNIPROT:Q14461; UNIPARC:UPI00000730D2; GB:M3505; GB:005465; NID:g18
A:Note: this sequence was not determined in this report; the translation is from an inco
C:Genetics:
A:Gene: GDB:GYPB
A:Cross-references: GDB:118891
A:Map position: 4q28-4q31

Query Match 27.8%; Score 20; DB 4; Length 13;
Best Local Similarity 66.7%; Pred. No. 2.6e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 SVKSLY 13
| | | | |
Db 7 STVSLY 12

RESULT 14

A61362
bradykinin-like peptide III - Japanese pond frog
C:Species: Rana nigromaculata (Japanese pond frog)
C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 05-Oct-2004

C:Accession: A61362

R:Nakajima, T.
Chem. Pharm. Bull. 16, 2088-2089, 1968
A:Title: On the third active peptide on smooth muscle in the skin of Rana nigromaculata
A:Reference number: A61362; MUID:69117202; PMID:5751736
A:Accession: A61362
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-14 <NAK>
A:Cross-references: UNIPROT:Q7LZ53; UNIPARC:UPI000017A4F1
C:Keywords: skin

Query Match 27.8%; Score 20; DB 2; Length 14;
Best Local Similarity 80.0%; Pred. No. 2.9e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PFSVA 6
| | | |
Db 7 PFRVA 11

RESULT 15

S68033
cytochrome P450 1A1 - tilapia (fragment)
C:Species: Oreochromis niloticus x Oreochromis aureus (tilapia)
C:Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 29-Aug-1997
C:Accession: S68033
R:Deng, Y.F.; Deng, T.H.
Arch. Biochem. Biophys. 322, 347-356, 1995
A:Title: Induction and purification of cytochrome P450 1A1 from 3-methylcholanthrene-tr
A:Reference number: S68033; MUID:96032654; PMID:7574707
A:Accession: S68033
A:Molecule type: protein
A:Residues: 1-10 <UEN>
A:Cross-references: UNIPARC:UPI000017CA77
A:Experimental source: liver and gill

Query Match 26.4%; Score 19; DB 2; Length 10;
Best Local Similarity 55.6%; Pred. No. 3.1e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 VPFSVAKSV 9
| | | | |
Db 2 LPTIGALSV 10

RESULT 16

B43669
hypothetical protein (rhdA 5' region) - Synecchococcus sp. (fragment)
C:Species: Synecchococcus sp.
C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 30-Sep-1993
C:Accession: B43669
R:Laudenbach, D.E.; Ehrhardt, D.; Green, L.; Grossman, A.
J. Bacteriol. 173, 2751-2760, 1991
A:Title: Isolation and characterization of a sulfur-regulated gene encoding a periplasm
A:Reference number: A43669; MUID:91210163; PMID:1708376
A:Accession: B43669
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-11 <LAU>
A:Cross-references: UNIPARC:UPI000017ABB7; GB:M65244

Query Match 26.4%; Score 19; DB 2; Length 11;
Best Local Similarity 57.1%; Pred. No. 3.4e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PFSVAKS 8
| | | | |
Db 2 PSSAAKN 8

RESULT 17

S26552

T-cell receptor beta chain (clone Cw3/701.1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 13-Jan-1995 #sequence_revision 17-Apr-1998 #ext_change 17-Mar-1999
C:Accession: S26552
R:Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid
J. Exp. Med. 176, 439-447, 1992
A:title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
A:Reference number: S26512; MUID:92364546; PMID:1380061
A:Accession: S26552
A:Molecule type: mRNA
A:Residues: 1-12 <CAS>
A:Cross-references: UNIPARC:UPI00001769C8; EMBL:X68002
A:Experimental source: cytolytic T-lymphocyte, clone Cw3/701.1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor

Query Match 26.4%; Score 19; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 KSLYLG 15
::|||
Db 7 ETLVFG 12

RESULT 18
S26549
T-cell receptor beta chain (clone Cw3/A8, Cw3/Cas1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 13-Jan-1995 #sequence_revision 17-Apr-1998 #ext_change 17-Mar-1999
C:Accession: S26549; S26550
R:Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid
J. Exp. Med. 176, 439-447, 1992
A:title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
A:Reference number: S26512; MUID:92364546; PMID:1380061
A:Accession: S26549
A:Molecule type: mRNA
A:Residues: 1-12 <CAS>
A:Cross-references: UNIPARC:UPI00001769C9; EMBL:X67999
A:Experimental source: cytolytic T-lymphocyte, clone Cw3/A8
A:Accession: S26550
A:Molecule type: mRNA
A:Residues: 1-12 <CA2>
A:Cross-references: UNIPARC:UPI00001769C9; EMBL:X68000
A:Experimental source: cytolytic T-lymphocyte, clone Cw3/Cas1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor

Query Match 26.4%; Score 19; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 KSLYLG 15
::|||
Db 7 ETLVFG 12

RESULT 19
S26553
T-cell receptor beta chain (clone Cw3/56.1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 13-Jan-1995 #sequence_revision 17-Apr-1998 #ext_change 17-Mar-1999
C:Accession: S26553
R:Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid
J. Exp. Med. 176, 439-447, 1992
A:title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
A:Reference number: S26512; MUID:92364546; PMID:1380061
A:Accession: S26553
A:Molecule type: mRNA
A:Residues: 1-12 <CAS>
A:Cross-references: UNIPARC:UPI00001769C6; EMBL:X68003
A:Experimental source: cytolytic T-lymphocyte, clone Cw3/56.1
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: T-cell receptor

Query Match 26.4%; Score 19; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 KSLYLG 15
::|||
Db 7 ETLVFG 12

RESULT 20
PH1469
T-cell receptor beta chain (clone A3/H2R2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #ext_change 15-Mar-2004
C:Accession: PH1469; S26551
R:Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Kc
J. Exp. Med. 177, 811-820, 1993
A:title: T cell receptor selection by and recognition of two class I major histocompatib
A:Reference number: PH1430; MUID:93171821; PMID:8436911
A:Accession: PH1469
A:Molecule type: mRNA
A:Residues: 1-12 <CAS>
A:Cross-references: UNIPARC:UPI000017C7A2
A:Experimental source: cytolytic T-lymphocyte, clone A3/H2R2
R:Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid
J. Exp. Med. 176, 439-447, 1992
A:title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
A:Reference number: S26512; MUID:92364546; PMID:1380061
A:Accession: S26551
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-12 <CA2>
A:Cross-references: UNIPARC:UPI000017C7A2; EMBL:X68001
A:Experimental source: cytolytic T-lymphocyte, clone Cw3/1F11
C:Keywords: receptor; T-cell

Query Match 26.4%; Score 19; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 KSLYLG 15
::|||
Db 7 ETLVFG 12

RESULT 21
S09721
2S albumin small chain nIII - rape (fragments)
C:Species: Brassica napus (rape)
C>Date: 19-Mar-1997 #sequence_revision 13-Mar-1998 #ext_change 13-Mar-1998
C:Accession: S09721
R:Monnaie, R.I.; Menendez-Arias, L.; Lopez-Otin, C.; Rodriguez, R.
FEBS Lett. 263, 209-212, 1990
A:title: beta-Turns as structural motifs for the proteolytic processing of seed proteins
A:Reference number: S09720; MUID:90242974; PMID:2185951
A:Accession: S09721
A:Molecule type: protein
A:Residues: 1-9;10-14 <MON>
A:Cross-references: UNIPARC:UPI000017B026; UNIPARC:UPI000017B027
A:Experimental source: seed

Query Match 26.4%; Score 19; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 4.4e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PPSVAK 7
|||
Db 4 PPRIPK 9

RESULT 22

A44920
2-halobenzoate 1,2-dioxygenase component A beta chain - Pseudomonas cepacia (fragment)
C/Species: Pseudomonas cepacia
C/Date: 01-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C/Accession: A44920
R/Fetzner, S.; Muller, R.; Lingens, F.
J. Bacteriol. 174, 279-290, 1992
A/Title: Purification and some properties of 2-halobenzoate 1,2-dioxygenase, a two-comp
A/Reference number: A44920; MUID:92104974; PMID:1370284
A/Contents: 2CBS
A/Accession: A44920
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-14 <P>
A/Cross-references: UNIPROT:Q9R506; UNIPARC:UPI000008BPBA
A/Note: sequence extracted from NCBI backbone (NCBIP:75379)

Query Match 26.4%; Score 19; DB 2; Length 14;
Best Local Similarity 57.1%; Pred. No. 4.4e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 SVKSLYL 14
Db 2 SLESSYL 8

RESULT 23
JN0859
peptidyl-dipeptidase A inhibitory peptide C105 - striped bonito
C/Species: Sarda orientalis (striped bonito)
C/Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999
C/Accession: JN0859
R/Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.
Bioeci. Biotechnol. Biochem. 57, 1743-1744, 1993
A/Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory pe
A/Reference number: JN0859; MUID:94080036; PMID:7764272
A/Accession: JN0859
A/Molecule type: protein
A/Residues: 1-7 <MAT>
A/Cross-references: UNIPARC:UPI00001566C2
A/Experimental source: intestine
C/Comment: The carboxyl-terminus is essential for the protein's expression of angiotensin
C/Superfamily: bradykinin-potentiating peptide
C/Keywords: angiotensin-converting enzyme inhibitor

Query Match 25.0%; Score 18; DB 2; Length 7;
Best Local Similarity 71.4%; Pred. No. 2.8e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 SVKSVK 10
Db 1 SVAKLEK 7

RESULT 24
A60624
angiotensin I - Japanese quail
C/Species: Coturnix coturnix japonica (Japanese quail)
C/Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 05-Oct-2004
C/Accession: A60624
R/Takel, Y.; Hasegawa, Y.
Gen. Comp. Endocrinol. 79, 12-22, 1990
A/Title: Vasopressor and depressor effects of native angiotensins and inhibition of the
A/Reference number: A60624; MUID:90284684; PMID:2191893
A/Accession: A60624
A/Molecule type: protein
A/Residues: 1-10 <TKA>
A/Cross-references: UNIPROT:P01018; UNIPARC:UPI0000035278
C/Superfamily: serpin
C/Keywords: blood pressure control; glycoprotein; liver; plasma; vasoconstrictor

Query Match 25.0%; Score 18; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 4.7e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PFSV 5
Db 7 PFSL 10

RESULT 25
A90917
angiotensin precursor - chicken (fragment)
C/Species: Gallus gallus (chicken)
C/Date: 30-Oct-1992 #sequence_revision 30-Oct-1992 #text_change 09-Jul-2004
C/Accession: A90917; A01250
R/Nakayama, T.; Nakajima, T.; Sokabe, H.
Chem. Pharm. Bull. 21, 2085-2087, 1973
A/Title: Comparative studies on angiotensins. III. Structure of fowl angiotensin and it
A/Reference number: A90917; MUID:74127845; PMID:4361802
A/Accession: A90917
A/Molecule type: protein
A/Residues: 1-10 <NAK>
A/Cross-references: UNIPROT:P01018; UNIPARC:UPI0000035278
C/Keywords: blood pressure control; hormone; vasoconstrictor
F/1-10/Product: angiotensin I #status experimental <ANI>
F/1-8/Product: angiotensin II #status experimental <AN2>

Query Match 25.0%; Score 18; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 4.7e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PFSV 5
Db 7 PFSL 10

RESULT 26
PH1375
T antigen variant K-2 - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 11-May-2000
C/Accession: PH1375
R/Lill, N.L.; Judith Tevethia, M.; Hendrickson, W.G.; Tevethia, S.S.
J. Exp. Med. 176, 449-457, 1992
A/Title: Cytotoxic T lymphocytes (CTL) against a transforming gene product select for t
A/Reference number: PH1373; MUID:92364547; PMID:1380062
A/Accession: PH1375
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-11 <LIL>
A/Cross-references: UNIPARC:UPI000017C758

Query Match 25.0%; Score 18; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 5.3e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 KSVKSLYL 14
Db 2 KGVNMYL 9

RESULT 27
S21163
NAD ADP-ribosyltransferase (EC 2.4.2.30) - rat (fragment)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 03-Jun-2002
C/Accession: S21163
R/Potvin, F.; Thibodeau, J.; Kirkland, J.B.; Dandenaault, B.; Duchaine, C.; Poirier, G.G.
FEBS Lett. 302, 269-273, 1992
A/Title: Structural analysis of the putative regulatory region of the rat gene encoding
A/Reference number: S21163; MUID:92290013; PMID:1601134
A/Accession: S21163
A/Molecule type: DNA
A/Residues: 1-12 <POT>
A/Cross-references: UNIPARC:UPI0000170AA3; EMBL:X65496; NID:G56847; PIDD:CAA46477.1; PIR

C;Keywords: glycosyltransferase; NAD; pentosyltransferase

Query Match 25.0%; Score 18; DB 2; Length 12;
Best Local Similarity 33.3%; Pred. No. 5.8e+03;
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 5 VAKSVKSLY 13
: ||| :
Db 1 MAEATERLY 9

RESULT 28

PH1463
T-cell receptor beta chain (clone A24/10.1) - mouse (fragment)

C;Species: Mus musculus (house mouse)
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 15-Mar-2004

C;Accession: PH1463

R;Caenova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannefier, C.; Regnault, A.; Kc
J. Exp. Med. 177, 811-820, 1993

A;Title: T cell receptor selection by and recognition of two class I major histocompatib
A;Reference number: PH1430; MUID:93171821; PMID:8436911

A;Accession: PH1463

A;Molecule type: mRNA

A;Residues: 1-12 <C&S>

A;Cross-references: UNIPARC:UPI000017C798

A;Experimental source: cytolytic T-lymphocyte

C;Keywords: receptor; T-cell

Query Match 25.0%; Score 18; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 5.8e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 SLYLG 15
: ||| :
Db 8 TLVFG 12

RESULT 29

PH1464
T-cell receptor beta chain (clone A3/63) - mouse (fragment)

C;Species: Mus musculus (house mouse)
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 15-Mar-2004

C;Accession: PH1464

R;Caenova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannefier, C.; Regnault, A.; Kc
J. Exp. Med. 177, 811-820, 1993

A;Title: T cell receptor selection by and recognition of two class I major histocompatib
A;Reference number: PH1430; MUID:93171821; PMID:8436911

A;Accession: PH1464

A;Molecule type: mRNA

A;Residues: 1-12 <C&S>

A;Cross-references: UNIPARC:UPI000017C79E

A;Experimental source: cytolytic T-lymphocyte

C;Keywords: receptor; T-cell

Query Match 25.0%; Score 18; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 5.8e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 SLYLG 15
: ||| :
Db 8 TLVFG 12

RESULT 30

PH1468
T-cell receptor beta chain - mouse (fragment)

C;Species: Mus musculus (house mouse)
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 15-Mar-2004

C;Accession: PH1468; PH1465

R;Caenova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannefier, C.; Regnault, A.; Kc
J. Exp. Med. 177, 811-820, 1993

A;Title: T cell receptor selection by and recognition of two class I major histocompatib
A;Reference number: PH1430; MUID:93171821; PMID:8436911

A;Accession: PH1468
A;Molecule type: mRNA
A;Residues: 1-12 <C&S1>

A;Cross-references: UNIPARC:UPI000017C7A9

A;Experimental source: cytolytic T-lymphocyte, clone A24/PER2

A;Accession: PH1465

A;Molecule type: mRNA

A;Residues: 1-12 <C&S2>

A;Cross-references: UNIPARC:UPI000017C7A9

A;Experimental source: cytolytic T-lymphocyte, clone 332/2G

C;Keywords: receptor; T-cell

Query Match 25.0%; Score 18; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 5.8e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 SLYLG 15
: ||| :
Db 8 TLVFG 12

RESULT 31

C60529
hemocyanin 1 - green crab (fragment)

C;Species: Carcinus maenas (green crab, common shore crab)
C;Date: 19-Mar-1993 #sequence_revision 19-Mar-1993 #text_change 09-Jul-2004

C;Accession: C60529

R;Neuteboom, B.; Sierdema, S.J.; Beintema, J.J.

Comp. Biochem. Physiol. B 94, 587-592, 1989

A;Title: The relationship between N-terminal sequences and immunological characterizatio

A;Reference number: A60529; MUID:90151075; PMID:2620501

A;Accession: C60529

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-12 <NEU>

A;Cross-references: UNIPROT:P83176; UNIPARC:UPI000012C375

Query Match 25.0%; Score 18; DB 2; Length 12;
Best Local Similarity 44.4%; Pred. No. 5.8e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 PFSVAKSVK 10
: ||| :
Db 3 PASVSDAKK 11

RESULT 32

S47384
T-cell antigen receptor VJ junction beta chain - human

C;Species: Homo sapiens (man)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999

C;Accession: S47384

R;Lehner, P.J.

submitted to the EMBL Data Library, August 1994

A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T c

A;Reference number: S47355

A;Accession: S47384

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-13 <LEH>

A;Cross-references: UNIPARC:UPI0000116689; EMBL:Z35704; NID:9527501; PIDN:CAA84773.1; PI

C;Keywords: T-cell receptor

Query Match 25.0%; Score 18; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 6.3e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 AKSVKSLY 13
: ||| :
Db 2 ASSRSRAV 9

RESULT 33

B61620
locustamyotropin IV - migratory locust
C/Species: Locusta migratoria (migratory locust)
C/Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 09-Jul-2004
C/Accession: B61620
R/Schoofs, L., Holman, G.M.; Hayes, T.K.; Nachman, R.J.; Kochansky, J.P.; De Loof, A.
Insect Biochem. Mol. Biol. 22, 447-452, 1992
A/Title: Isolation, identification and synthesis of locustamyotropin III and IV, two add
A/Reference number: A61620
A/Accession: B61620
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-13 <SCH>
A/Cross-references: UNIPROT:P41490; UNIPARC:UPI000012E792
C/Keywords: amidated carboxyl end; neuropeptide
F/13/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 25.0%; Score 18; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 6.3e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFS 4
DB 7 MPFS 10

RESULT 34
NYPG14
hypothalamic tetradecapeptide - pig
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 09-Jul-2004
C/Accession: A01419
R/Schlesinger, D.H.; Niall, H.D.; Linthicum, G.L.; Dupont, A.; Schally, A.V.
submitted to the Atlas, November 1976
A/Reference number: A01419
A/Accession: A01419
A/Molecule type: protein
A/Residues: 1-14 <SCH>
A/Cross-references: UNIPROT:P01155; UNIPARC:UPI000012CFC3
C/Keywords: amidated carboxyl end; hypothalamus
F/14/Modified site: amidated carboxyl end (Tyr) #status experimental

Query Match 25.0%; Score 18; DB 1; Length 14;
Best Local Similarity 55.6%; Pred. No. 6.8e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 AKSVKSLYL 14
DB 1 ARYKSPYL 9

RESULT 35
B59137
protein PFI - golden needle mushroom (fragment)
C/Species: Flammulina velutipes (golden needle mushroom)
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: B59137
R/Sakamoto, Y.; Ando, A.; Tamai, Y.; Miura, K.
submitted to the Protein Sequence Database, November 1999
A/Description: Differences of proteins expressed in the fruiting dikaryon and the non-fr
A/Reference number: A59137
A/Accession: B59137
A/Molecule type: protein
A/Residues: 1-15 <SKA>
A/Cross-references: UNIPROT:Q7M4X0; UNIPARC:UPI000017CB23
A/Experimental source: strain FV-4

Query Match 25.0%; Score 18; DB 2; Length 15;
Best Local Similarity 60.0%; Pred. No. 7.3e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VPFSV 5

DB 9 VPMSI 13

RESULT 36
PC2132
FMRamide-related heptapeptide - Panagrellus redivivus
C/Species: Panagrellus redivivus
C/Date: 03-May-1994 #sequence_revision 15-Oct-1994 #text_change 09-Jul-2004
C/Accession: PC2132
R/Maule, A.G.; Shaw, C.; Bowman, J.W.; Halton, D.W.; Thompson, D.P.; Geary, T.G.; Thim,
Biochem. Biophys. Res. Commun. 200, 973-980, 1994
A/Title: KSAVMRFamide: a novel FMRamide-related heptapeptide from the free-living nema
A/Reference number: PC2132; MUID:94235053; PMID:8179635
A/Accession: PC2132
A/Molecule type: protein
A/Residues: 1-7 <MAU>
A/Cross-references: UNIPROT:P41874; UNIPARC:UPI000003AD32
C/Keywords: amidated carboxyl end
F/7/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 23.6%; Score 17; DB 2; Length 7;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 KSLYL 14
DB 1 KSAVM 5

RESULT 37
A13687
caerulein-like peptide - African tree frog (Kaasina maculata)
C/Species: Kaasina maculata
C/Date: 13-Mar-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C/Accession: A13687
R/Montecucchi, P.; Falconieri Erspamer, G.; Visser, J.
Experientia 33, 1138-1139, 1977
A/Title: Occurrence of Asn(2), Leu(5)-caerulein in the skin of the African frog Hylandat
A/Reference number: A13687; MUID:77246547; PMID:891852
A/Accession: A13687
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-10 <MON>
A/Cross-references: UNIPROT:Q7LZC5; UNIPARC:UPI000017668C
C/Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid; skin; sulfoliprotein
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F/4/Binding site: sulfate (Tyr) (covalent) #status experimental
F/10/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 23.6%; Score 17; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 YLG 15
DB 4 YLG 6

RESULT 38
C39745
sphingomyelinase - Rhodococcus sp. (fragment)
C/Species: Rhodococcus sp.
C/Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 30-Sep-1993
C/Accession: C39745
R/Ito, M.; Ikegami, Y.; Yamagata, T.
J. Biol. Chem. 266, 7919-7926, 1991
A/Title: Activator proteins for glycosphingolipid hydrolysis by endoglycoceramidases. E
ble using these activator proteins.
A/Reference number: A39745; MUID:91210321; PMID:1850427
A/Accession: C39745
A/Status: preliminary

A:Molecule type: protein
A:Residues: 1-10 <ITO>
A:Cross-references: UNIPARC:UPI000017AD7A

Query Match 23.6%; Score 17; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 7.3e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VPFSVA 6
|||
Db 4 LPASTA 9

RESULT 39

B49164
Chromogranin-B - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 31-Oct-1997
C:Accession: B49164
R:Nielsen, E.; Welinder, B.S.; Madsen, O.D.
Endocrinology 129, 3147-3156, 1991

A:Title: Chromogranin-B, a putative precursor of eight novel rat glucagonoma peptides th
A:Reference number: A49164; MUID:92063871; PMID:1954895

A:Accession: B49164
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-11 <NIE>
A:Cross-references: UNIPARC:UPI00000E7128
A:Note: sequence extracted from NCBI backbone (NCBI:66370)
C:Superfamily: chromogranin B precursor

Query Match 23.6%; Score 17; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PFS 4
|||
Db 1 PFS 3

RESULT 40

PC2372
58K heat shock protein groEL [similarity] - Bacillus cereus (strain ts-4) (fragment)
C:Species: Bacillus cereus
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: PC2372
R:Matsumoto, K.; Miyamoto, T.; Yamaguchi, K.; Sayed, M.A.; Kajiwara, T.; Hatanaka, S.
Bioest. Biotechnol. Biochem. 59, 231-235, 1995
A:Title: Identification of DNA-binding proteins changed after induction of sporulation i
A:Reference number: PC2369; MUID:95218265; PMID:7766022

A:Accession: PC2372
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-11 <MAS>
A:Cross-references: UNIPARC:UPI000017AC8A
C:Keywords: heat shock; molecular chaperone; stress-induced protein

Query Match 23.6%; Score 17; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 AKSVK 10
|||
Db 1 AKDIK 5

RESULT 41

S43957
Ig mu chain V region (clone 3) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 20-Oct-1994 #sequence_revision 26-Jul-1996 #text_change 17-Mar-1999
C:Accession: S43957
R:Wagner, S.D.; Williams, G.T.; Larson, T.; Neuburger, M.S.; Kitamura, D.; Rajewsky, K.

Nucleic Acids Res. 22, 1389-1393, 1994
A:Title: Antibodies generated from human immunoglobulin miniloci in transgenic mice.
A:Reference number: S43956; MUID:94248036; PMID:8190629

A:Accession: S43957
A:Molecule type: DNA
A:Residues: 1-12 <WAG>
A:Cross-references: UNIPARC:UPI000017C26A
C:Keywords: immunoglobulin

Query Match 23.6%; Score 17; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PFSV 5
|||
Db 5 PFDV 8

RESULT 42

PH0785
T-cell receptor alpha chain (OAI1.3.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PH0785
R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991

A:Title: T cell receptor genes in a series of class I major histocompatibility complex-r
allelic exclusion and antigen-specific repertoire.
A:Reference number: PH0746; MUID:92078846; PMID:1836010

A:Accession: PH0785
A:Molecule type: mRNA
A:Residues: 1-12 <CRNA>
A:Cross-references: UNIPARC:UPI000017C781; EMBL:X60887
A:Experimental source: T lymphocyte
C:Keywords: T-cell receptor

Query Match 23.6%; Score 17; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 LVLG 15
|||
Db 9 LTFG 12

RESULT 43

P00696
1,4-alpha-glucan branching enzyme (EC 2.4.1.18) [imported] - rice (fragment)
C:Species: Oryza sativa (rice)
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: P00696
R:Komatsu, S.; Kajiwara, H.; Hirano, H.
Theor. Appl. Genet. 86, 935-942, 1993

A:Title: A rice protein library; a data-file of rice proteins separated by two-dimension
A:Reference number: P00696
A:Accession: P00696
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-12 <KOM>

A:Cross-references: UNIPROT:O7M284; UNIPARC:UPI000017B0EC
C:Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

Query Match 23.6%; Score 17; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 8.9e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 PFSV 5
|||
Db 6 PFNI 9

RESULT 44

PT0263

Ig heavy chain CRD3 region (clone 2-121B) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0263
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: PT0222; MID:91108337; PMID:1899102
A:Accession: PT0263
A:Molecule type: DNA
A:Residues: 1-13 <YAM>
A:Cross-references: UNIPARC:UPI000017C1F0
A:Experimental source: B lymphocyte
C:Keywords: heterotrimer; immunoglobulin

Query Match 23.6%; Score 17; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 YLG 15
|||
Db 9 YLG 11

RESULT 45
S47356
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47356
R:Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A:Reference number: S47355
A:Accession: S47356
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: UNIPARC:UPI0000116676; EMBL:Z35680; NID:G527449; PIDN:CAA84749.1; PI
C:Keywords: T-cell receptor

Query Match 23.6%; Score 17; DB 2; Length 13;
Best Local Similarity 36.4%; Pred. No. 9.7e+03;
Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 SVAKSKSLYL 14
|:|:|
Db 3 SSTRSTDYQL 13

RESULT 46
S47359
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47359
R:Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A:Reference number: S47355
A:Accession: S47359
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: UNIPARC:UPI0000116679; EMBL:Z35683; NID:G527455; PIDN:CAA84752.1; PI
C:Keywords: T-cell receptor

Query Match 23.6%; Score 17; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 9.7e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 AKSVKSLY 13
|:|:|

Db 2 ASSSRSSY 9

RESULT 47
S47371
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47371
R:Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A:Reference number: S47355
A:Accession: S47371
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: UNIPARC:UPI0000116683; EMBL:Z35696; NID:G527483; PIDN:CAA84765.1; PI
C:Keywords: T-cell receptor

Query Match 23.6%; Score 17; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 9.7e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 AKSVKS 11
|:|:|
Db 2 ASSIRS 7

RESULT 48
S47373
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47373
R:Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A:Reference number: S47355
A:Accession: S47373
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: UNIPARC:UPI0000116671; EMBL:Z35672; NID:G527489; PIDN:CAA84741.1; PI
C:Keywords: T-cell receptor

Query Match 23.6%; Score 17; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 9.7e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 AKSVKS 11
|:|:|
Db 2 ASSIRS 7

RESULT 49
S47380
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47380
R:Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A:Reference number: S47355
A:Accession: S47380
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: UNIPARC:UPI0000116672; EMBL:Z35673; NID:G527511; PIDN:CAA84742.1; PI
C:Keywords: T-cell receptor

Query Match 23.6%; Score 17; DB 2; Length 13;

Best Local Similarity 50.0%; Pred. No. 9.7e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 6 AKSVKS 11
DB 2 ASSIRS 7

RESULT 50

S47390
T-cell antigen receptor VI junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47390
R:Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A:Reference number: S47355
A:Accession: S47390
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: UNIPARC:UPI0000116688; EMBL:Z35703; NID:G527459; PIDN:CAA84772.1; PI
C:Keywords: T-cell receptor

Query Match 23.6%; Score 17; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 9.7e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 AKSVKS 11
DB 2 ASSIRS 7

RESULT 51

S47392
T-cell antigen receptor VI junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47392
R:Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A:Reference number: S47355
A:Accession: S47392
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: UNIPARC:UPI0000116690; EMBL:Z35713; NID:G527521; PIDN:CAA84782.1; PI
C:Keywords: T-cell receptor

Query Match 23.6%; Score 17; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 9.7e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 AKSVKS 11
DB 2 ASSIRS 7

RESULT 52

S20578
ribosomal protein L36 - Cryptomonas sp. chloroplast (fragment)
C:Species: Chloroplast Cryptomonas sp.
C:Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
C:Accession: S20578
R:Douglas, S.E.
FEBS Lett. 298, 93-96, 1992
A:Title: A secY homologue is found in the plastid genome of Cryptomonas Ph.
A:Reference number: S20577; MUID:92183838; PMID:1544427
A:Accession: S20578
A:Molecule type: DNA
A:Residues: 1-13 <DOU>

A:Cross-references: UNIPROT:P28528; UNIPARC:UPI000017AED5; EMBL:X62348; NID:G11300; PID
A>Note: the source is designated as Cryptomonas phi
C:Genetics:
A:Gene: rpl36
A:Genome: chloroplast
C:Keywords: chloroplast

Query Match 23.6%; Score 17; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 9.7e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 VAKSVKSL 12
DB 3 VVSSIGSL 10

RESULT 53

JZVHPI
crabrolin - European hornet
C:Species: Vespa crabro (European hornet)
C:Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 16-Aug-2004
C:Accession: A01781
R:Argiolas, A.; Pisano, J.J.
J. Biol. Chem. 259, 10106-10111, 1984
A:Title: Isolation and characterization of two new peptides, mastoparan C and crabrolin,
A:Reference number: A92441; MUID:84289390; PMID:6206053
A:Accession: A01781
A:Molecule type: protein
A:Residues: 1-13 <ARG>
A:Cross-references: UNIPROT:P01518; UNIPARC:UPI00001283DB
C:Comment: This cytoactive peptide from hornet venom induces mast cell degranulation.
C:Keywords: amidated carboxyl end; venom
F.13/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 23.6%; Score 17; DB 2; Length 13;
Best Local Similarity 33.3%; Pred. No. 9.7e+03;
Matches 4; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 VPFSAKSVKSL 12
DB 2 LPLIRKIVTAL 13

RESULT 54

QMVHP2
mastoparan C - European hornet
C:Species: Vespa crabro (European hornet)
C:Date: 28-Feb-1986 #sequence_revision 28-Feb-1986 #text_change 09-Jul-2004
C:Accession: A01779
R:Argiolas, A.; Pisano, J.J.
J. Biol. Chem. 259, 10106-10111, 1984
A:Title: Isolation and characterization of two new peptides, mastoparan C and crabrolin,
A:Reference number: A92441; MUID:84289390; PMID:6206053
A:Accession: A01779
A:Molecule type: protein
A:Residues: 1-14 <ARG>
A:Cross-references: UNIPROT:P01516; UNIPARC:UPI000012EBD3
C:Comment: This cytoactive peptide from hornet venom induces mast cell degranulation.
C:Superfamily: mastoparan
C:Keywords: amidated carboxyl end; venom
F.14/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 23.6%; Score 17; DB 1; Length 14;
Best Local Similarity 50.0%; Pred. No. 1e+04;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 SVAKSV 9
DB 8 AVAKKI 13

RESULT 55

PA0015

seed storage protein 12S 2 - Arabidopsis thaliana (fragment)

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 11-Jul-1997

C/Accession: PA0015

R/Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.

submitted to JIPID, July 1994

A/Description: Separation and characterization of Arabidopsis proteins by two-dimensional

A/Reference number: PA0001

A/Accession: PA0015

A/Molecule type: protein

A/Residues: 1-14 <KAM>

A/Cross-references: UNIPARC:UPI000017B010

A/Experimental source: seed

C/Keywords: pyroglutamic acid; seed; storage protein

F:/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match

Best Local Similarity 23.6%; Score 17; DB 2; Length 14;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 13 YLG 15

DB 3 YLG 5

RESULT 56

PT0223

Ig heavy chain CDR3 region (clone 1-88B) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C/Accession: PT0223

R/Yamada, M.; Masserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and

A/Reference number: PT0222; MUID:91108337; PMID:189102

A/Accession: PT0223

A/Molecule type: DNA

A/Residues: 1-14 <YAM>

A/Cross-references: UNIPARC:UPI000017C1D5

A/Experimental source: B lymphocyte

C/Keywords: heterotetramer; immunoglobulin

Query Match

Best Local Similarity 23.6%; Score 17; DB 2; Length 14;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPF 3

DB 5 VPF 7

RESULT 57

S36678

dodecenoyl-CoA Delta-isomerase (EC 5.3.3.8) / enoyl-CoA hydratase (EC 4.2.1.17) / 3-hydro

C/Species: Mus musculus (house mouse)

C/Date: 19-Mar-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004

C/Accession: S36678

R/Chen, N.; Crane, D.I.

Biochem. J. 283, 605-610, 1992

A/Title: Induction of the major integral membrane protein of mouse liver peroxisomes by

A/Reference number: S21285; MUID:92246895; PMID:1575703

A/Accession: S36678

A/Molecule type: protein

A/Residues: 1-14 <CHE>

A/Cross-references: UNIPROT:Q7M0B0; UNIPARC:UPI000017C652

A/Experimental source: liver

C/Function:

A/Pathway: fatty acid beta-oxidation

C/Keywords: carbon-oxygen lyase; fatty acid beta-oxidation; hydro-lyase; intramolecular

Query Match

Best Local Similarity 23.6%; Score 17; DB 2; Length 14;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PFSSVA 6

DB 7 PFRVS 11

RESULT 58

LFECF

phe operon leader peptide - Escherichia coli (strain K-12)

N/Alternate names: attenuator peptide

C/Species: Escherichia coli

C/Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004

C/Accession: A03593; B36494; A65038

R/Zurawski, G.; Brown, K.; Killingly, D.; Yanofsky, C.

Proc. Natl. Acad. Sci. U.S.A. 75, 4271-4275, 1978

A/Title: Nucleotide sequence of the leader region of the phenylalanine operon of Escher

A/Reference number: A03593; MUID:79033820; PMID:360214

A/Accession: A03593

A/Molecule type: DNA

A/Residues: 1-15 <ZUR>

A/Cross-references: UNIPROT:P03057; UNIPARC:UPI000012E851; GB:V00314; GB:J01658; NID:94

R/Gavini, N.; Davidson, B.E.

J. Biol. Chem. 265, 21532-21535, 1990

A/Title: phea mutants of Escherichia coli have a defective phea attenuator.

A/Reference number: A36494; MUID:91072346; PMID:2254312

A/Accession: B36494

A/Molecule type: DNA

A/Residues: 1-15 <GAV>

A/Cross-references: UNIPARC:UPI000012E851; GB:M58024; GB:J05694; NID:9147178; PIDN:AAA6

R/Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C.

A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A/Title: The complete genome sequence of Escherichia coli K-12.

A/Reference number: A64720; MUID:97426617; PMID:9278503

A/Accession: A65038

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-15 <BLAT>

A/Cross-references: UNIPARC:UPI000012E851; GB:AE00346; GB:U00956; NID:92367141; PIDN:A

A/Experimental source: strain K-12, substrain MG1655

C/Genetics:

A/Gene: phea, phea

A/Map position: 56 min

C/Superfamily: phea leader peptide

Query Match

Best Local Similarity 23.6%; Score 17; DB 1; Length 15;

Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 VPFSSVA 6

DB 4 IPFFPA 9

RESULT 59

PH0784

T-cell receptor alpha chain (P1) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C/Accession: PH0784

R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991

A/Title: T cell receptor gene in a series of class I major histocompatibility complex-

allelic exclusion and antigen-specific repertoire

A/Reference number: PH0746; MUID:92078846; PMID:1836010

A/Accession: PH0784

A/Molecule type: mRNA

A/Residues: 1-15 <CAS>

A/Cross-references: UNIPARC:UPI000017C76B; EMBL:X60885

A/Experimental source: T lymphocyte

C/Keywords: T-cell receptor

Query Match

Best Local Similarity 23.6%; Score 17; DB 2; Length 15;

Best Local Similarity 75.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 12 LYLIG 15
|||
12 LYFG 15
Db

RESULT 60

PH0797
T-cell receptor alpha chain (PF2.10.1 V-alpha-3.AR5) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PH0797
R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A:Title: T cell receptor genes in a series of class I major histocompatibility complex-
allelic exclusion and antigen-specific repertoire.
A:Reference number: PH0746; MUID:92078846; PMID:1836010
A:Accession: PH0797
A:Molecule type: mRNA
A:Residues: 1-15 <CAS>
A:Cross-references: UNIPARC:UPI0000117C780; EMBL:X60903
A:Experimental source: T lymphocyte
C:Keywords: T-cell receptor

Query Match 23.6%; Score 17; DB 2; Length 15;
Best Local Similarity 25.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 4 SVAKSVKSLYLIG 15
|||
4 SITGNTRKLIIG 15
Db

RESULT 61

PH0750
T-cell receptor beta chain (C11) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PH0750
R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A:Title: T cell receptor genes in a series of class I major histocompatibility complex-
allelic exclusion and antigen-specific repertoire.
A:Reference number: PH0746; MUID:92078846; PMID:1836010
A:Accession: PH0750
A:Molecule type: mRNA
A:Residues: 1-15 <CAS>
A:Cross-references: UNIPARC:UPI0000115FA9; EMBL:X06841
A:Experimental source: T lymphocyte
C:Keywords: T-cell receptor

Query Match 23.6%; Score 17; DB 2; Length 15;
Best Local Similarity 75.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 LYLIG 15
|||
12 LYFG 15
Db

RESULT 62

PH0751
T-cell receptor beta chain (F12) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C:Accession: PH0751
R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A:Title: T cell receptor genes in a series of class I major histocompatibility complex-
allelic exclusion and antigen-specific repertoire.
A:Reference number: PH0746; MUID:92078846; PMID:1836010

A:Accession: PH0751
A:Molecule type: mRNA
A:Residues: 1-15 <CAS>
A:Cross-references: UNIPARC:UPI0000115FA9; EMBL:X60843; NID:G50931; PIDN:CAA43235.1; PIC
A:Experimental source: T lymphocyte
C:Keywords: T-cell receptor

Query Match 23.6%; Score 17; DB 2; Length 15;
Best Local Similarity 75.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 LYLIG 15
|||
12 LYFG 15
Db

RESULT 63

S77987
cytochrome-c oxidase (EC 1.9.3.1) chain vic.2 - bigeye tuna (fragments)
C:Species: Thunnus obesus (bigeye tuna)
C:Date: 17-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C:Accession: S77987
R:Arnold, S.; Lee, J.; Kim, M.; Song, E.; Linder, D.; Lotzpeich, F.; Kadenbach, B.
submitted to the Protein Sequence Database, June 1997
A:Reference number: S77980
A:Accession: S77987
A:Molecule type: protein
A:Residues: 1-8;9-15 <ARN>
A:Cross-references: UNIPROT:P80978; UNIPARC:UPI000017BF73; UNIPARC:UPI000017BF74
A:Experimental source: heart
C:Genetics:
A:Genome: nuclear
A:Function:
A:Pathway: oxidative phosphorylation; respiratory chain
C:Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane

Query Match 23.6%; Score 17; DB 2; Length 15;
Best Local Similarity 55.6%; Pred. No. 1.1e+04;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 VAKSVKSLYLIG 13
|||
6 VAKKPMSPDY 14
Db

RESULT 64

A41436
alpha-macroglobulin - green sea turtle (fragment)
C:Species: Chelonia mydas (green sea turtle)
C:Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 09-Jul-2004
C:Accession: A41436
R:Osada, T.; Sasaki, T.; Imai, A.
J. Biochem. 103, 212-217, 1988
A:Title: Purification and characterization of alpha-macroglobulin and ovomacroglobulin o
A:Reference number: A41436; MUID:88227890; PMID:2453503
A:Accession: A41436
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <OSA>
A:Cross-references: UNIPROT:Q7LZ35; UNIPARC:UPI000017BFB3

Query Match 23.6%; Score 17; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPF 3
|||
10 VPF 12
Db

RESULT 65

A61140
sperm acrosomal protein - spoonworm (Urechis caupo) (fragment)

C/Species: Urechis caupo
C/Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-Apr-1994
C/Accession: A61140
R/Gould, M.C.; Stephano, J.L.
Dev. Biol. 146, 509-518, 1991
A/Title: Peptides from sperm acrosomal protease that initiate egg development.
A/Reference number: A61140; MUID:91323672; PMID:1864468
A/Accession: A61140
A/Molecule type: protein
A/Residues: 1-6 <GOU>
A/Cross-references: UNIPARC:UPI000017BD8D

Query Match 22.2%; Score 16; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 VAKSVK 10
|||
Db 1 VAKKPK 6

RESULT 66

C24180
Fibrinogen beta chain - Japanese macaque (fragment)
N/Contains: fibrinopeptide B
C/Species: Macaca fuscata (Japanese macaque)
C/Date: 05-Jun-1988 #sequence_revision 10-Mar-1994 #text_change 09-Jul-2004
C/Accession: C24180
R/Nakamura, S.; Takenaka, O.; Takahashi, K.
J. Biochem. 97, 1487-1492, 1985
A/Title: Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and patas monkey (E. venosus) and baboons.
A/Reference number: A91990; MUID:85289140; PMID:3928610
A/Accession: C24180
A/Molecule type: protein
A/Residues: 1-9 <NAK>
A/Cross-references: UNIPROT:P19345; UNIPARC:UPI000012A77B
C/Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide

Query Match 22.2%; Score 16; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 10 KSLYLK 15
|||
Db 3 ESLFSG 8

RESULT 67

PC7073
ubiquinol-cytochrome-c reductase (EC 1.10.2.2) core protein II - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C/Accession: PC7073
R/Tsugita, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Matsui, T.; Watanabe, Y.;
Electrophoresis 21, 1853-1871, 2000
A/Title: Proteome analysis of mouse brain: Two-dimensional electrophoresis profiles of
A/Reference number: PC7072
A/Accession: PC7073
A/Molecule type: protein
A/Residues: 1-9 <TSU>
A/Cross-references: UNIPROT:Q9CVK7; UNIPARC:UPI000017CDE7
C/Keywords: brain; core protein; oxidoreductase

Query Match 22.2%; Score 16; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 VAKSVK 10
|||
Db 4 VAKKPK 9

RESULT 68
PC4442
Cytochrome c553 - Desulfovibrio desulfuricans (fragment)
C/Species: Desulfovibrio desulfuricans
C/Date: 28-Mar-1998 #sequence_revision 28-Mar-1998 #text_change 09-Jul-2004
C/Accession: PC4442
R/Abbert, C.; Leroy, G.; Bianco, P.; Forest, E.; Bruschi, M.; Dolla, A.
Biochem. Biophys. Res. Commun. 242, 213-218, 1998
A/Title: Characterization of the cytochromes C from Desulfovibrio desulfuricans G201.
A/Reference number: PC4442; MUID:98102811; PMID:9439638
A/Accession: PC4442
A/Molecule type: protein
A/Residues: 1-10 <AUB>
A/Cross-references: UNIPROT:Q7M0M6; UNIPARC:UPI000017AB62
A/Experimental source: strain G201
C/Comment: This protein is involved in the formate reduction pathway.

Query Match 22.2%; Score 16; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.1e+04;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 6 AKSVKSLY 13
|||
Db 1 AEDGASLY 8

RESULT 69

PU0029
33K protein 3218 - rice (strain Nohonbare) (fragment)
C/Species: Oryza sativa (rice)
C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 11-Apr-1995
C/Accession: PU0029
R/Tsugita, A.; Miyake, N.
Submitted to JIPID, April 1993
A/Reference number: PS0208
A/Accession: PU0029
A/Molecule type: protein
A/Residues: 1-11 <TSU>
A/Cross-references: UNIPARC:UPI000017B0FE
A/Experimental source: bran
C/Comment: molecular weight 33K, pI 6.0.

Query Match 22.2%; Score 16; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 PFSV 5
|||
Db 6 PFXI 9

RESULT 70

S58244
pyrrolquinoline quinone synthase C - Pseudomonas fluorescens (fragment)
C/Species: Pseudomonas fluorescens
C/Date: 11-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C/Accession: S58244
R/Schneider, U.; Keel, C.; Defago, G.; Haas, D.
Submitted to the EMBL Data Library, May 1995
A/Description: Tn5-directed cloning of pqd genes from Pseudomonas fluorescens CHA0: the
A/Reference number: S58239
A/Accession: S58244
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-11 <SCH>
A/Cross-references: UNIPROT:P55173; UNIPARC:UPI0000132130; EMBL:X87299; NID:G929799; PI

Query Match 22.2%; Score 16; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 PFSVAK 7
|||

Db 5 PLUSAE 10

RESULT 71

H84082

hypothetical protein BH3464 [imported] - *Bacillus halodurans* (strain C-125)

C:Species: *Bacillus halodurans*

C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004

C:Accession: H84082

R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira

Nucleic Acids Res. 28, 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and

A:Reference number: A83650; MUID:20512582; PMID:11058132

A:Accession: H84082

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-11 <STO>

A:Cross-references: UNIPROT:Q9K7A4; UNIPARC:UP100000C41E3; GB:AP001518; GB:BA000004; NID

A:Experimental source: strain C-125

C:Genetics:

A:Gene: BH3464

Query Match 22.2%; Score 16; DB 2; Length 11;

Best Local Similarity 57.1%; Pred. No. 1.2e+04;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 VKSLVYG 15

Db 3 VKELLSG 9

RESULT 72

S00616

parasporal crystal protein, wax moth-specific - *Bacillus thuringiensis* (strain galleriae

N:Alternate names: delta-endotoxin; parasporal crystal protein positive chain

C:Species: *Bacillus thuringiensis*

C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 05-Oct-2004

C:Accession: S00616

R:Chetukhina, G.G.; Kostina, L.I.; Zalunin, I.A.; Khodova, O.M.; Stepanov, V.M.

FEBS Lett. 232, 249-251, 1988

A:Title: *Bacillus thuringiensis* ssp. *galleriae* simultaneously produces two delta-endotox

A:Reference number: S00615

A:Accession: S00616

A:Molecule type: protein

A:Residues: 1-11 <CHE>

A:Cross-references: UNIPROT:Q7M54; UNIPARC:UP100001781A1

C:Comment: This toxin is effective against the larvae of *Galleria mellonella* (greater wax

C:Keywords: delta-endotoxin

Query Match 22.2%; Score 16; DB 2; Length 11;

Best Local Similarity 60.0%; Pred. No. 1.2e+04;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PSVA 6

Db 7 PYSQA 11

RESULT 73

LFECPE

pyrE leader peptide - *Escherichia coli*

C:Species: *Escherichia coli*

C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004

C:Accession: A30400; A05110; Q00495

R:Poulsen, P.; Bonekamp, F.; Jensen, K.F.

EMBO J. 3, 1783-1790, 1984

A:Title: Structure of the *Escherichia coli* pyrE operon and control of pyrE expression by

A:Reference number: A30400; MUID:85003588; PMID:6207018

A:Accession: A30400

A:Molecule type: DNA

A:Residues: 1-12 <POU>

A:Cross-references: UNIPROT:P17776; UNIPARC:UP1000013C2E1

R:Poulsen, P.; Jensen, K.F.; Valentin-Hansen, P.; Carlsson, P.; Lundberg, L.G.

Eur. J. Biochem. 135, 223-229, 1983

A:Title: Nucleotide sequence of the *Escherichia coli* pyrE gene and of the DNA in front

A:Reference number: A05110; MUID:83287414; PMID:6349599

A:Accession: A05110

A:Molecule type: DNA

A:Residues: 1-12 <POU>

A:Cross-references: UNIPARC:UP1000013C2E1

C:Genetics:

A:Gene: pyrE-lp

C:Superfamily: pyrE leader peptide

Query Match 22.2%; Score 16; DB 1; Length 12;

Best Local Similarity 37.5%; Pred. No. 1.4e+04;

Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 PSVAKSVK 10

Db 5 FVCRKVR 12

RESULT 74

A28856

fructose-bisphosphate aldolase (EC 4.1.2.13) B, hepatic - rabbit (fragment)

C:Species: *Oryctolagus cuniculus* (domestic rabbit)

C:Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 31-Oct-1997

C:Accession: A28856

R:Hamappel, E.; MacGregor, J.S.; Davoust, S.; Horecker, B.L.

Arch. Biochem. Biophys. 214, 293-298, 1982

A:Title: Limited proteolysis of liver and muscle aldolases: effects of subtilisin, cathe

A:Reference number: A28856; MUID:82205113; PMID:7044315

A:Accession: A28856

A:Molecule type: protein

A:Residues: 1-12 <HAN>

A:Cross-references: UNIPARC:UP10000175FP2

C:Superfamily: fructose-bisphosphate aldolase

C:Keywords: aldehyde-lyase; carbon-carbon lyase; gluconeogenesis; glycolysis; liver; pen

Query Match 22.2%; Score 16; DB 2; Length 12;

Best Local Similarity 50.0%; Pred. No. 1.4e+04;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 SVKSLV 13

Db 1 STQSLF 6

RESULT 75

S47362

T-cell antigen receptor VJ junction beta chain - human

C:Species: *Homo sapiens* (man)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999

C:Accession: S47362

R:Lehner, P.J.

submitted to the EMBL Data Library, August 1994

A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T c

A:Reference number: S47355

A:Accession: S47362

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-13 <LEH>

A:Cross-references: UNIPARC:UP1000011667E; EMBL:Z35688; NID:gs27465; PIDN:CAA84757.1; PI

C:Keywords: T-cell receptor

Query Match 22.2%; Score 16; DB 2; Length 13;

Best Local Similarity 66.7%; Pred. No. 1.5e+04;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AKSVKS 11

Db 2 ASVSVS 7

RESULT 76
S47368
T-cell antigen receptor VJ junction beta chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C/Accession: S47368
R/Lehner, P.J.
Submitted to the EMBL Data Library, August 1994
A/Description: Human HLA-A*0201 restricted recognition of influenza A is dominated by T
A/Reference number: S47355
A/Accession: S47368
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-13 <LEH>
A/Cross-references: UNIPARC:UPI0000116681; EMBL:Z35693; NID:9527477; PIDN:CAA84762.1; PI
C/Keywords: T-cell receptor

Query Match 22.2%; Score 16; DB 2; Length 13;
Best Local Similarity 37.5%; Pred. No. 1.5e+04;
Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 6 AKSVKSLY 13
DB 2 ASSTRGAY 9

RESULT 77
S47400
T-cell antigen receptor VJ junction beta chain - human
C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C/Accession: S47400
R/Lehner, P.J.
Submitted to the EMBL Data Library, August 1994
A/Description: Human HLA-A*0201 restricted recognition of influenza A is dominated by T
A/Reference number: S47355
A/Accession: S47400
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-13 <LEH>
A/Cross-references: UNIPARC:UPI0000116675; EMBL:Z35678; NID:9527535; PIDN:CAA84747.1; PI
C/Keywords: T-cell receptor

Query Match 22.2%; Score 16; DB 2; Length 13;
Best Local Similarity 30.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 SVAKSVKSLY 13
DB 4 SVALATEAFF 13

RESULT 78
A60336
outer membrane protein OmpA homolog - Actinobacillus actinomycetemcomitans (fragment)
C/Species: Actinobacillus actinomycetemcomitans
C/Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 31-Dec-2004
C/Accession: A60336
R/Wilson, M.E.
Infect. Immun. 59, 2505-2507, 1991
A/Title: The heat-modifiable outer membrane protein of Actinobacillus actinomycetemcomit
A/Reference number: A60336; MUID:91267635; PMID:2050416
A/Accession: A60336
A/Molecule type: protein
A/Residues: 1-13 <WIL>
A/Cross-references: UNIPROT:Q9S5U9; UNIPROT:O51841; UNIPARC:UPI00001780B0
C/Keywords: membrane protein

Query Match 22.2%; Score 16; DB 2; Length 13;
Best Local Similarity 30.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 6 AKSVKSLYLG 15

DB 1 APQANTEYAG 10

RESULT 79
S13864
methyl coenzyme M reductase (EC 1.8.-.-) II alpha chain - Methanobacterium thermoautotro
C/Species: Methanobacterium thermoautotrophicum
A/Variety: strain Marburg
C/Date: 19-Mar-1997 #sequence_revision 13-Sep-1998 #text_change 30-Oct-1998
C/Accession: S13864
R/Rosper, S.; Linder, D.; Ellermann, J.; Thauer, R.K.
Eur. J. Biochem. 194, 871-877, 1990
A/Title: Two genetically distinct methyl-coenzyme M reductases in Methanobacterium cher
A/Reference number: S13864; MUID:9109370; PMID:2269306
A/Accession: S13864
A/Molecule type: protein
A/Residues: 1-14 <ROS>
A/Cross-references: UNIPARC:UPI000012EDDF
A/Experimental source: strain Marburg
C/Keywords: methanogenesis; oxidoreductase

Query Match 22.2%; Score 16; DB 2; Length 14;
Best Local Similarity 60.0%; Pred. No. 1.6e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 KSLY 14
DB 4 KKLFL 8

RESULT 80
S11074
alcohol dehydrogenase (EC 1.1.1.1) - Baltic cod (fragments)
C/Species: Gadus morhua callarias (Baltic cod)
C/Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 31-Jan-1997
C/Accession: S11074
R/Begstad, B.; Estenius, M.; Danielsson, O.; Persson, B.; Cedertund, E.; Kaiser, R.; Ho
FBBS Lett. 269, 194-196, 1990
A/Title: Fast atom bombardment mass spectrometry and chemical analysis in determinati
A/Reference number: S11074; MUID:90353571; PMID:2387402
A/Accession: S11074
A/Molecule type: protein
A/Residues: 1-5,6-14 <RGE>
A/Cross-references: UNIPARC:UPI000017BF65; UNIPARC:UPI000017BF66
C/Keywords: acetylated amino end; alcohol metabolism; NAD; oxidoreductase
F/1/Modified site: acetylated amino end (Ala) #status experimental

Query Match 22.2%; Score 16; DB 2; Length 14;
Best Local Similarity 22.2%; Pred. No. 1.6e+04;
Matches 2; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 4 SVAKSVKSL 12
DB 2 TVGKCIRTV 10

Search completed: July 12, 2006, 05:39:44
Job time : 46 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 12, 2006, 05:30:49 ; Search time 293 Seconds
(without alignments)
47.356 Million cell updates/sec

Title: US-10-671-019-2

Perfect score: 72
Sequence: 1 VPFSAKSVKSLYLIG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 8966

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 800 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	34.7	14	2 Q7M4W9	FLAVE
2	24	33.3	15	2 Q798U8	STROK
3	23	31.9	10	1 MDAR2	SOYBN
4	23	31.9	14	1 CRBL	VESSOR
5	23	31.9	14	2 OSGIT6	ASPL
6	23	31.9	14	2 Q7M487	ANDAU
7	23	31.9	14	2 Q3TU57	MOUSE
8	22	30.6	8	2 P82858	GBASI
9	22	30.6	8	2 P92386	HORWA
10	22	30.6	14	2 Q6E0X9	YEAST
11	22	30.6	15	1 ASPI	LACSN
12	22	30.6	15	1 P83331	STRTR
13	21	29.2	8	2 P92215	AGRCR
14	21	29.2	8	2 P92222	BROIN
15	21	29.2	8	2 P92227	CRIDE
16	21	29.2	8	2 P92373	GRIDE
17	21	29.2	8	2 P92382	GRIDE
18	21	29.2	8	2 P92384	GRIDE
19	21	29.2	8	2 P92388	GRIDE
20	21	29.2	8	2 P92391	HERPI
21	21	29.2	8	2 P92394	HORVU
22	21	29.2	8	2 P92404	LOPEL
23	21	29.2	8	2 P92422	PSAPR
24	21	29.2	8	2 P92426	PSEPI
25	21	29.2	8	2 P92428	PSOAL
26	21	29.2	8	2 P92431	AEGRF
27	21	29.2	8	2 P92441	THREB
28	21	29.2	8	2 P92443	TAECM
29	21	29.2	8	2 P93955	FESFE
30	21	29.2	8	2 P93957	FESSE
31	21	29.2	8	2 P93957	FESSE

32	21	29.2	8	2 P93959	9POL
33	21	29.2	8	2 P93961	PSARU
34	21	29.2	8	2 P93963	PSAST
35	21	29.2	8	2 P93965	SECT
36	21	29.2	8	2 P93966	AEOSP
37	21	29.2	8	2 P93970	9POL
38	21	29.2	8	2 P93973	EREDL
39	21	29.2	8	2 P93981	9POL
40	21	29.2	8	2 P93985	AEOSM
41	21	29.2	8	2 P93992	AUSVE
42	21	29.2	9	2 Q5EFY1	9BRIO
43	21	29.2	9	2 Q5EFY7	9BRIO
44	21	29.2	9	2 Q5EFZ0	9BRIO
45	21	29.2	10	2 Q3YLM8	STRAB
46	21	29.2	12	2 Q31851	ARATH
47	21	29.2	14	2 Q714T5	SCRIP
48	21	29.2	14	2 Q85662	REOVJ
49	21	29.2	15	2 Q9UC22	HUMAN
50	21	29.2	15	2 Q4X416	PLACH
51	21	29.2	15	2 Q714T8	9FLOR
52	20	27.8	10	2 Q755J5	MEUR
53	20	27.8	10	2 P83161	ANASL
54	20	27.8	11	2 Q53VR5	MOUSE
55	20	27.8	11	2 Q86866	9VIRU
56	20	27.8	11	2 Q86868	9VIRU
57	20	27.8	12	1 HCVB	MECCR
58	20	27.8	12	2 Q945C3	CRICO
59	20	27.8	12	2 Q6VSD4	9PLAR
60	20	27.8	13	1 UPE71	LITEN
61	20	27.8	13	1 Q14461	HUMAN
62	20	27.8	14	1 BRK3	RANR1
63	20	27.8	14	1 HCV3	MECCR
64	20	27.8	14	2 Q96050	HUMAN
65	20	27.8	15	2 Q38ZU5	LACSS
66	19	26.4	8	2 Q70Y88	9PLAT
67	19	26.4	9	2 Q6UQ3	MACCU
68	19	26.4	9	2 Q6U7P3	RALBU
69	19	26.4	10	2 Q47651	ECOLI
70	19	26.4	11	2 Q9UCP2	HUMAN
71	19	26.4	11	2 Q59AK1	9COLS
72	19	26.4	12	2 Q5U1X7	9FLOR
73	19	26.4	12	2 Q6PAJ9	MOUSE
74	19	26.4	13	1 DAH11	LITDA
75	19	26.4	13	1 SAHH1	POPEU
76	19	26.4	13	1 SAHH2	POPEU
77	19	26.4	13	2 Q97122	TOXCO
78	19	26.4	13	2 Q9U7D6	NEOCA
79	19	26.4	13	2 Q50038	MYCLE
80	19	26.4	14	2 Q4XAS9	PLACH
81	19	26.4	14	2 Q5U7U8	9FLOR
82	19	26.4	14	2 Q9R5O6	BURCE
83	19	26.4	14	2 Q78EC9	RAT
84	19	26.4	15	1 CWP14	PHAVU
85	19	26.4	15	1 CWP16	TOBAC
86	19	26.4	15	2 Q5U1X3	9FLOR
87	18	25.7	15	2 Q571P1	ABRPV
88	18	25.0	10	1 ANGT	CHICK
89	18	25.0	10	1 ANGT	COTUA
90	18	25.0	10	2 Q7WUG1	PSEFL
91	18	25.0	11	2 Q2KKK1	9BRIO
92	18	25.0	11	2 Q707P1	RAT
93	18	25.0	11	2 Q77893	ORENI
94	18	25.0	12	1 HCV1	CARMA
95	18	25.0	12	2 Q6KEF1	HUMAN
96	18	25.0	12	2 Q7KYL7	HUMAN
97	18	25.0	12	2 Q7RNA6	PLAYO
98	18	25.0	12	2 Q3ZBX8	BOVIN
99	18	25.0	12	2 Q8SBL1	BPR69
100	18	25.0	12	2 Q4KUI2	9FLOR
101	18	25.0	12	2 Q4KUI4	9FLOR
102	18	25.0	12	2 Q4KUI8	9FLOR
103	18	25.0	12	2 Q4KUI9	9FLOR
104	18	25.0	12	2 Q4KUK0	9FLOR

P93959	hordeum ere
P93961	psathyrosta
P93963	psathyrosta
P93965	secta
P93966	aequilops
P93970	eremopyrum
P93973	eremopyrum
P93981	eremopyrum
P93985	aequilops co
P93992	aequilops co
Q5EFY1	polycichum
Q5EFY7	cedipodium
Q5EFZ0	buxbaumia a
Q3YLM8	strix aluco
Q31851	arabidopsis
Q714T5	rhodomonas
Q85662	reovirus ty
Q9UC22	homo sapien
Q4X416	plasmidium
Q714T8	masid.alfus
Q755J5	neurospora
P83161	anabena. sp
Q53VR5	mus muschlu
Q86866	lymphocytic
Q86868	lymphocytic
Q10584	megathura c
Q945C3	cryptocodi
Q6VSD4	thalassoma
P82050	litoria ewi
Q14461	homo sapien
Q71253	rana nigrom
Q10583	megathura c
Q96050	homo sapien
Q38ZU5	lactobacilli
Q70Y88	platostoma
Q6UQ3	macaca mula
Q6U7P3	ralesonia e
Q47651	escherichia
Q9UCP2	homo sapien
Q59AK1	cicindela (
Q5U1X7	gracilaria
Q6PAJ9	mus musculu
DAH11	litoria dah
SAHH1	populus eup
SAHH2	populus eup
Q97122	toxoplasma
Q9U7D6	neospora ca
Q50038	mycobacteri
Q4XAS9	plasmidium
Q5U7U8	gracilaria
Q9R5O6	burkholderi
Q78EC9	ratus norv
P80793	phaseolus v
P80793	nicotiana t
Q5U1X3	gracilaria
Q571P1	aeromonas p
P67885	gallus gall
P67886	colurnix co
Q7WUG1	pseudomonas
Q2KKK1	fissidens s
Q707P1	ratus norv
Q77893	oreochromis
P83176	carcinus ma
Q6KEF1	homo sapien
Q7KYL7	homo sapien
Q7RNA6	plasmidium
Q3ZBX8	bos taurus
Q8SBL1	bacterioph
Q4KUI2	gracieloupa
Q4KUI4	gracieloupa
Q4KUI8	gracieloupa
Q4KUI9	gracieloupa
Q4KUK0	gracieloupa

105	18	25.0	12	2	Q4KUK4_9FLOR	Q4kuk4 grateuloupia	178	17	23.6	12	2	Q6VSE8_9LABR	Q6vee8 thalassoma
106	18	25.0	12	2	Q8SEB8_9FLOR	Q8seb8 grateuloupia	179	17	23.6	12	2	Q6VSE9_9LABR	Q6vef1 thalassoma
107	18	25.0	12	2	Q8SEB9_9FLOR	Q8seb9 grateuloupia	180	17	23.6	12	2	Q6VSP1_9LABR	Q6vef1 thalassoma
108	18	25.0	13	1	CRBL_VESLE	P1723 vesputia lew	181	17	23.6	12	2	Q6VSP2_9LABR	Q6vef2 thalassoma
109	18	25.0	13	1	DAH12_LITDA	P84263 litorea dan	182	17	23.6	12	2	Q6VSP3_9LABR	Q6vef3 thalassoma
110	18	25.0	13	1	LMT4_LOCM1	P4190 locustia mig	183	17	23.6	12	2	Q6VSP4_9LABR	Q6vef4 thalassoma
111	18	25.0	13	1	VG16_BACSU	P80867 bacillus su	184	17	23.6	12	2	Q6VSP5_9LABR	Q6vef5 thalassoma
112	18	25.0	13	2	Q8WKG0_HUMAN	Q8wkg0 homo sapien	185	17	23.6	12	2	Q6VSP6_GOMVA	Q6vef6 gomphosus v
113	18	25.0	13	2	Q6EUS5_STREBO	Q6eus5 streptococc	186	17	23.6	12	2	Q5A8XH6_9HTV1	Q5a8x6 human immun
114	18	25.0	13	2	Q6LCB1_RAT	Q6lcb1 rattus norv	187	17	23.6	12	2	Q5A8XH8_9HTV1	Q5a8x8 human immun
115	18	25.0	14	1	FEET_TOBAC	P82150 nicotiana t	188	17	23.6	12	2	Q5A8X10_9HTV1	Q5a8x10 human immun
116	18	25.0	14	1	HY14_PPG	P01155 sus scrofa	189	17	23.6	12	2	Q5EETV0_9HTV1	Q5eetv0 human immun
117	18	25.0	14	2	Q4XJ52_PLACH	Q4xj52 plasmodium	190	17	23.6	12	2	Q5EETV4_9HTV1	Q5eetv4 human immun
118	18	25.0	14	2	Q69ES5_STREBO	Q69es5 streptococc	191	17	23.6	12	2	Q5EETV6_9HTV1	Q5eetv6 human immun
119	18	25.0	15	1	HSP11_FINPS	P81083 pinus pinas	192	17	23.6	12	2	Q5EETV8_9HTV1	Q5eetv8 human immun
120	18	25.0	15	2	Q7M4X0_FLAWE	Q7m4x0 flammulina	193	17	23.6	12	2	Q5EETZ0_9HTV1	Q5eetz0 human immun
121	18	25.0	15	2	Q95OP6_9PUNG	Q95op6 rhizophydlu	194	17	23.6	12	2	Q5EUT04_9HTV1	Q5eut04 human immun
122	18	25.0	15	2	Q71GVO_9HME	Q71gvo andrena teg	195	17	23.6	12	2	Q5EU06_9HTV1	Q5eu06 human immun
123	18	25.0	15	2	Q9TRM3_BOVIN	Q9trm3 bos taurus	196	17	23.6	12	2	Q5EU08_9HTV1	Q5eu08 human immun
124	18	25.0	15	2	Q9TRM8_PIG	Q9trm8 sus scrofa	197	17	23.6	12	2	Q5EU14_9HTV1	Q5eu14 human immun
125	18	25.0	15	2	Q4GXZ9_ECOLI	Q4gxz9 escherichia	198	17	23.6	12	2	Q5EU16_9HTV1	Q5eu16 human immun
126	18	25.0	15	2	Q5D4R7_9CYAN	Q5d4r7 oscillatori	199	17	23.6	12	2	Q5EUI8_9HTV1	Q5eui8 human immun
127	18	25.0	15	2	Q9OZC9_MOUSE	Q9ocz9 mus musculi	200	17	23.6	12	2	Q5EUI8_9HTV1	Q5eui8 human immun
128	17	25.0	15	2	MAST_ANTPM	P0C022 anterhychni	201	17	23.6	12	2	Q5EUI8_9HTV1	Q5eui8 human immun
129	17	23.6	7	1	PAR3_HABCO	P81298 haemophilus	202	17	23.6	12	2	Q5EUI8_9HTV1	Q5eui8 human immun
130	17	23.6	7	1	PAR3_PANRE	P41874 panagrellus	203	17	23.6	12	2	Q5EUI3_9HTV1	Q5eui3 human immun
131	17	23.6	8	1	UC24_MAIZE	P80630 zea mays (m	204	17	23.6	12	2	Q5EUI3_9HTV1	Q5eui3 human immun
132	17	23.6	8	1	PPK3_PERAM	P82618 periplaneta	205	17	23.6	12	2	Q5EUI3_9HTV1	Q5eui3 human immun
133	17	23.6	8	1	Q9XNP8_BOOMI	Q9xnp8 boophilus m	206	17	23.6	12	2	Q5EUI3_9HTV1	Q5eui3 human immun
134	17	23.6	9	1	JELL3_APIME	P84759 apis mellif	207	17	23.6	12	2	Q5EUI3_9HTV1	Q5eui3 human immun
135	17	23.6	9	2	Q4YEF1_PLABE	Q4yef1 plasmodium	208	17	23.6	13	1	Q5EUI3_9HTV1	Q5eui3 human immun
136	17	23.6	9	2	Q3YAP7_MACMU	Q3yap7 macaca mula	209	17	23.6	13	1	Q5EUI3_9HTV1	Q5eui3 human immun
137	17	23.6	9	2	Q359S3_MOUSE	Q359s3 mus musculi	210	17	23.6	13	2	Q5EUI3_9HTV1	Q5eui3 human immun
138	17	23.6	9	2	Q7ZP19_9HTV1	Q7zpj9 human immun	211	17	23.6	13	2	Q5EUI3_9HTV1	Q5eui3 human immun
139	17	23.6	9	2	Q7ZP19_9HTV1	Q7zpj9 human immun	212	17	23.6	14	1	MAST_VESCR	Q5a892 homo sapien
140	17	23.6	9	2	Q7ZPJ3_9HTV1	Q7zpj3 human immun	213	17	23.6	14	1	MAST_VESCR	Q5a892 homo sapien
141	17	23.6	9	2	Q7ZPJ3_9HTV1	Q7zpj3 human immun	214	17	23.6	14	2	Q61CK3_HUMAN	P01516 vespa crabr
142	17	23.6	9	2	Q7ZPJ7_9HTV1	Q7zpj7 human immun	215	17	23.6	14	2	Q61CK3_HUMAN	Q61ck3 homo sapien
143	17	23.6	9	2	Q7ZPK1_9HTV1	Q7zpk1 human immun	216	17	23.6	14	2	Q61WS6_HUMAN	Q61ws6 homo sapien
144	17	23.6	10	1	ANOP_ANOSM	P0C005 anopliis sa	217	17	23.6	14	2	Q4X3A3_PLACH	Q4x3a3 plasmodium
145	17	23.6	10	1	RIP_LUPAC	P84530 luffa acuta	218	17	23.6	14	2	Q4Y7R1_PLACH	Q4y7r1 plasmodium
146	17	23.6	10	2	Q5O843_METVO	Q5o843 methanococc	219	17	23.6	14	2	Q4Y9M8_PLABE	Q4y9m8 plasmodium
147	17	23.6	10	2	Q5R2U3_HUMAN	Q5r2u3 homo sapien	220	17	23.6	14	2	Q71GX0_9HME	Q71gx0 andrena zef
148	17	23.6	10	2	Q4YFM5_PLABE	Q4yfm5 plasmodium	221	17	23.6	14	2	Q311U6_HYLLA	Q311u6 hylobates l
149	17	23.6	10	2	Q71UL3_HALRU	Q71ul3 halictus ru	222	17	23.6	14	2	Q9WRP6_9POLA	Q9wrp6 hodeum mur
150	17	23.6	10	2	Q3YL50_STRAB	Q3yl50 strix aluco	223	17	23.6	14	2	Q5FPAN5_CAMLA	Q5fpan5 campylobact
151	17	23.6	10	2	Q7LZC5_KASMA	Q7lzc5 kassia mac	224	17	23.6	15	1	Q7M0B0_MOUSE	Q7m0b0 mus muscu
152	17	23.6	11	2	Q9TOR6_BPMU	Q9tor6 bacterioph	225	17	23.6	15	1	Q5EUI3_9HTV1	P80770 phaseolus v
153	17	23.6	11	2	Q9OVH3_9MORI	Q9ovh3 rattus sp.	226	17	23.6	15	1	Q5EUI3_9HTV1	P80978 thunnus ooe
154	17	23.6	11	2	Q86864_9VIRU	Q86864 lymphocytic	227	17	23.6	15	1	Q5EUI3_9HTV1	P06d73 escherichia
155	17	23.6	11	2	UKA2_HUMAN	P31144 homo sapien	228	17	23.6	15	1	Q4W671_LEMED	P06d73 shigella fi
156	17	23.6	12	2	Q7RH69_PLAYO	Q7rh69 plasmodium	229	17	23.6	15	2	Q4W671_LEMED	Q71a41 homo sapien
157	17	23.6	12	2	Q6JDM4_CANFA	Q6jdm4 canis famli	230	17	23.6	15	2	Q6JDM4_CANFA	Q6jdm4 homo sapien
158	17	23.6	12	2	Q4KUK6_9FLOR	Q4kuk6 grateuloupia	231	17	23.6	15	2	Q6JDM4_CANFA	Q6jdm4 homo sapien
159	17	23.6	12	2	Q7M284_ORYSA	Q7m284 oryza sativ	232	17	23.6	15	2	Q6JDM4_CANFA	Q6jdm4 homo sapien
160	17	23.6	12	2	Q8SEB7_9FLOR	Q8seb7 grateuloupia	233	17	23.6	15	2	Q6JDM4_CANFA	Q6jdm4 homo sapien
161	17	23.6	12	2	Q35868_MOUSE	Q35868 mus musculi	234	17	23.6	15	2	Q6JDM4_CANFA	Q6jdm4 homo sapien
162	17	23.6	12	2	Q6VSD1_9LABR	Q6vsd1 thalassoma	235	17	23.6	15	2	Q6VSD1_9LABR	Q6vsd1 thalassoma
163	17	23.6	12	2	Q6VSD2_9LABR	Q6vsd2 thalassoma	236	17	23.6	15	2	Q6VSD2_9LABR	Q6vsd2 thalassoma
164	17	23.6	12	2	Q6VSD3_9LABR	Q6vsd3 thalassoma	237	17	23.6	15	2	Q6VSD3_9LABR	Q6vsd3 thalassoma
165	17	23.6	12	2	Q6VSD5_9LABR	Q6vds5 thalassoma	238	17	23.6	15	2	Q6VSD5_9LABR	Q6vds5 thalassoma
166	17	23.6	12	2	Q6VSD6_9LABR	Q6vds6 thalassoma	239	17	23.6	15	2	Q6VSD6_9LABR	Q6vds6 thalassoma
167	17	23.6	12	2	Q6VSD7_9LABR	Q6vds7 thalassoma	240	17	23.6	15	2	Q6VSD7_9LABR	Q6vds7 thalassoma
168	17	23.6	12	2	Q6VSD8_9LABR	Q6vds8 thalassoma	241	17	23.6	15	2	Q6VSD8_9LABR	Q6vds8 thalassoma
169	17	23.6	12	2	Q6VSD9_9LABR	Q6vds9 thalassoma	242	17	23.6	15	2	Q6VSD9_9LABR	Q6vds9 thalassoma
170	17	23.6	12	2	Q6VSE0_9LABR	Q6ves0 thalassoma	243	17	23.6	15	2	Q6VSE0_9LABR	Q6ves0 thalassoma
171	17	23.6	12	2	Q6VSE1_9LABR	Q6ves1 thalassoma	244	17	23.6	15	2	Q6VSE1_9LABR	Q6ves1 thalassoma
172	17	23.6	12	2	Q6VSE2_9LABR	Q6ves2 thalassoma	245	17	23.6	15	2	Q6VSE2_9LABR	Q6ves2 thalassoma
173	17	23.6	12	2	Q6VSE3_9LABR	Q6ves3 thalassoma	246	17	23.6	15	2	Q6VSE3_9LABR	Q6ves3 thalassoma
174	17	23.6	12	2	Q6VSE4_9LABR	Q6ves4 thalassoma	247	17	23.6	15	2	Q6VSE4_9LABR	Q6ves4 thalassoma
175	17	23.6	12	2	Q6VSE5_9LABR	Q6ves5 thalassoma	248	17	23.6	15	2	Q6VSE5_9LABR	Q6ves5 thalassoma
176	17	23.6	12	2	Q6VSE6_9LABR	Q6ves6 thalassoma	249	17	23.6	15	2	Q6VSE6_9LABR	Q6ves6 thalassoma
177	17	23.6	12	2	Q6VSE7_9LABR	Q6ves7 thalassoma	250	17	23.6	15	2	Q6VSE7_9LABR	Q6ves7 thalassoma

251	16	22.2	10	2	Q75SW3_ECOLI	Q75sw3 escherichia	324	16	22.2	15	1	CKX_WHEAT	P58763 triticum ae
252	16	22.2	10	2	Q7MOM6_DESDE	Q7mom6 desulfovibr	325	16	22.2	15	1	CMPI8_TOBAC	P80795 nicotiana t
253	16	22.2	11	1	POOC_PSEFL	P55113 pseudomonas	326	16	22.2	15	1	MPPI8_FAT	P81563 rattus norv
254	16	22.2	11	1	PVK1_BLACK	P83923 blaberus cr	327	16	22.2	15	2	Q9UWH4_GEURU	Q9uwh4 pyrococcus.
255	16	22.2	11	1	PVK1_BLAU	P83924 blaberus cr	328	16	22.2	15	2	P82207_BOMMO	Q4y13 bombyx mori
256	16	22.2	11	1	PVK1_BLAGI	P84565 cyrtoceria gi	329	16	22.2	15	2	Q4YIV3_PLABE	Q4yiv3 plasmodium
257	16	22.2	11	1	PVK1_CYROPO	P84656 cyrtoceria p	330	16	22.2	15	2	Q7M3B4_VULVU	Q7m3b4 vulpus vulp
258	16	22.2	11	1	PVK1_GROPO	P83925 gromphadori	331	16	22.2	15	2	Q7TRG9_BOVIN	Q7trg9 bos taurus
259	16	22.2	11	1	PVK1_LEUMA	P83921 leucophaea	332	16	22.2	15	2	Q5XPT1_SOLUT	Q5xpt1 solanum tub
260	16	22.2	11	1	PVK1_MALCI	P83922 nauphaea c	333	16	22.2	15	2	Q05463_9PROT	Q05463 nitrosopir
261	16	22.2	11	1	PVK1_PERVV	P84657 periphaeri	334	16	22.2	15	2	P97249_9PROT	P97249 nitrosopir
262	16	22.2	11	1	PVK3_PYCSU	P84654 pycnoscelus	335	16	22.2	15	2	Q8LI61_THERB	Q8li61 thermoaner
263	16	22.2	11	1	PVK3_APRFU	P84661 aptera fusc	336	16	22.2	15	2	Q9RSP2_SERMA	Q9rsp2 seriatia ma
264	16	22.2	11	1	PVK3_BLACK	P83923 blaberus cr	337	16	22.2	15	2	Q86128_9RHA	Q86128 vesicular s
265	16	22.2	11	1	PVK3_BLAU	P84563 blaberus gi	338	16	22.2	15	2	Q9PKX5_TEV	Q9pkx5 tubacco etc
266	16	22.2	11	1	PVK3_BLAGI	P84565 cyrtoceria gi	339	16	22.2	15	2	Q91Y24_MOUSE	Q91y24 mus musculu
267	16	22.2	11	1	PVK3_GROPO	P83925 gromphadori	340	15.5	21.5	15	1	UCI7_MAIZE	Q9yq10 zea mays (m
268	16	22.2	11	1	PVK3_LEUMA	P83921 leucophaea	341	15	20.8	8	1	CCRN_DRAVI	Q9yq10 transmissib
269	16	22.2	11	1	PVK3_MALCI	P84662 panchlora v	342	15	20.8	8	1	CCRN_MACEU	P86125 dasyvurus vi
270	16	22.2	11	1	PVK3_PANVI	Q31b66 candidarus	343	15	20.8	8	1	CONO_CONMU	P86126 macrophis eu
271	16	22.2	11	2	Q3LBZ6_9MOUL	Q7m154 bacillus th	344	15	20.8	8	1	NS3_MYCTU	P84701 conus mus (
272	16	22.2	11	2	Q9K7A4_BACRU	Q9k7a4 bacillus ha	345	15	20.8	8	1	P82324_PEA	P81152 mycobacteri
273	16	22.2	11	2	XYLA_STRVN	P14405 streptomyce	346	15	20.8	8	2	Q30822_AEGTA	P82324 pisum sativ
274	16	22.2	12	1	YZPY_ECOLI	P17776 escherichia	347	15	20.8	9	2	Q71EB9_HUMAN	Q30822 aegilops ta
275	16	22.2	12	2	Q68CUI_HUMAN	Q68cui homo sapien	348	15	20.8	9	2	Q71EB9_HUMAN	Q71eb9 homo sapien
276	16	22.2	12	2	Q47251_ECOLI	Q47251 escherichia	349	15	20.8	9	2	Q4YIG1_PLABE	Q4yig1 plasmodium
277	16	22.2	12	2	Q8A4V9_9ENMR	Q8a4v9 buchnera ap	350	15	20.8	9	2	Q7M2N8_BOSIN	Q7m2n8 bos indicus
278	16	22.2	12	2	Q69232_BHVA	Q69232 bovine heip	351	15	20.8	9	2	Q4S852_CLOBU	Q4s852 clostridium
279	16	22.2	12	2	Q3B742_BRARE	Q3b742 brachydanio	352	15	20.8	9	2	Q6LDP7_RAT	Q6ldp7 rattus norv
280	16	22.2	12	2	Q4PU25_9CICH	Q4pu25 neolamprolo	353	15	20.8	10	1	CPM03_TOBAC	P84664 citrys gamb
281	16	22.2	12	2	Q4PU26_9CICH	Q4pu26 neolamprolo	354	15	20.8	10	2	SC41_FITCA	Q7s1h4 neurospora
282	16	22.2	12	2	Q4PU27_9CICH	Q4pu27 lepidiolamp	355	15	20.8	10	2	Q4XZ43_PLACH	Q4xz43 plasmodium
283	16	22.2	12	2	Q4PU29_9CICH	Q4pu29 juldoctrom	356	15	20.8	10	2	Q7RH60_PLAVO	Q7rh60 plasmodium
284	16	22.2	12	2	Q4PU30_9CICH	Q4pu30 neolamprolo	357	15	20.8	10	2	Q8WPL6_9URCO	Q8wpl6 altopleura
285	16	22.2	12	2	Q4PU31_9CICH	Q4pu31 lepidiolamp	358	15	20.8	10	2	Q38217_9CAUD	Q38217 laccococcus
286	16	22.2	12	2	Q4PU32_9CICH	Q4pu32 lepidiolamp	359	15	20.8	10	2	Q56ZK9_ARATH	Q56zk9 arabidopsis
287	16	22.2	12	2	Q4PU33_9CICH	Q4pu33 lepidiolamp	360	15	20.8	10	2	Q7MOK7_RHOSO	Q7mok7 rhodococcus
288	16	22.2	12	2	Q4PU34_9CICH	Q4pu34 altoplamprol	361	15	20.8	10	2	Q71YN2_MOUSE	Q71yn2 mus musculu
289	16	22.2	12	2	Q4PU35_9CICH	Q4pu35 lepidiolamp	362	15	20.8	10	2	Q9ES07_ALMAT	Q9es07 alligator m
290	16	22.2	12	2	Q4PU41_9CICH	Q4pu41 lepidiolamp	363	15	20.8	10	2	BRKP_PHYSA	Q71252 phyllomedus
291	16	22.2	12	2	Q4PU31_9CICH	Q4pu31 lamprolagus	364	15	20.8	11	1	KNL2_PHYSA	P84667 phyllomedus
292	16	22.2	12	2	Q4PU37_ALTEL	Q4pu37 altoplamprol	365	15	20.8	11	1	TKN_ELECI	P62933 eleone cir
293	16	22.2	12	2	Q4PU42_9CICH	Q4pu42 lepidiolamp	366	15	20.8	11	1	TKN_ELECI	P62934 eleone mos
294	16	22.2	12	2	Q4PU44_9CICH	Q4pu44 lepidiolamp	367	15	20.8	11	1	TKN_ELECI	Q4x9y5 plasmodium
295	16	22.2	12	2	Q213J6_CHAGU	Q213j6 champsoceph	368	15	20.8	11	2	Q4X9Y5_PLACH	Q4x9y5 plasmodium
296	16	22.2	12	2	Q65027_AYINB	Q65027 avian myelo	369	15	20.8	11	2	Q4Z2C6_PLABE	Q4z2c6 plasmodium
297	16	22.2	13	1	AH4_PRUSE	P29262 prunus sero	370	15	20.8	11	2	Q9XSP2_HYLSY	Q9xsp2 hylobates s
298	16	22.2	13	1	AUR11_LITRA	P82386 littoria ran	371	15	20.8	11	2	Q9XSP5_PANTR	Q9xsp5 pan troglod
299	16	22.2	13	1	AUR12_LITRA	P82387 littoria ran	372	15	20.8	11	2	Q9XSP6_PONPY	Q9xsp6 pongo pygma
300	16	22.2	13	1	RS19_ASHYP	Q44592 ash yellow	373	15	20.8	11	2	Q9XSP7_PYGNE	Q9xsp7 pygathrix n
301	16	22.2	13	1	TE1GC_RANCL	P82882 rana clamit	374	15	20.8	11	2	Q9XSP8_9PRIM	Q9xsp8 preblytis j
302	16	22.2	13	2	P87031_YEAST	P87031 baccharomyc	375	15	20.8	11	2	Q9XSP4_9PRIM	Q9xsp4 gorilla gor
303	16	22.2	13	2	Q7RSC5_PLAVO	Q7res5 plasmodium	376	15	20.8	11	2	Q6T352_QUEPE	Q6t352 quepus pet
304	16	22.2	13	2	Q32XJ6_PLEA	Q32xj6 plecotus ra	377	15	20.8	11	2	Q70Y70_9LAMI	Q70y70 thornicrofti
305	16	22.2	13	2	Q7BVK6_ERWAM	Q7bv6 erwania amy	378	15	20.8	11	2	Q7TME3_MOUSE	Q7tme3 mus musculu
306	16	22.2	13	2	Q8GBU2_VIBHA	Q8gbu2 vibrio harv	379	15	20.8	11	2	Q77892_ORENI	Q77892 oreochromis
307	16	22.2	13	2	Q9AMK2_XANCP	Q9amk2 xanthomonas	380	15	20.8	11	2	Q77906_ORENI	Q77906 oreochromis
308	16	22.2	13	2	Q9RRZ4_MYCNC	Q9rrz4 mycoplasma	381	15	20.8	12	1	VESE_VESXA	Q7m1c2 vespa manda
309	16	22.2	13	2	Q9RG00_MYCCA	Q9rg00 mycoplasma	382	15	20.8	12	1	VESE_VESXA	Q7m1c2 vespa xanth
310	16	22.2	13	2	P90442_NPVSL	P90442 spodoptera	383	15	20.8	12	2	Q9UMR0_HUMAN	Q9umr0 homo sapien
311	16	22.2	14	1	HBX_OREMO	P83761 oreochromis	384	15	20.8	12	2	Q4Y2T2_PLACH	Q4y2t2 plasmodium
312	16	22.2	14	1	MCRX_METTM	P58815 methanobact	385	15	20.8	12	2	Q9BFV4_MYRTR	Q9bfv4 myriecophag
313	16	22.2	14	1	PLYBI_POLPI	P84388 polybia pau	386	15	20.8	12	2	Q70Y67_9LAMI	Q70y67 proctantther
314	16	22.2	14	1	PLYB2_POLPI	P84389 polybia pau	387	15	20.8	12	2	Q70Y95_9LAMI	Q70y95 ociumu giat
315	16	22.2	14	1	TKN1_SCHGR	P82470 schistocerc	388	15	20.8	12	2	Q8S1G4_9CALI	Q8s1g4 halymenta f
316	16	22.2	14	1	Q96KF9_HUMAN	Q96kf9 homo sapien	389	15	20.8	12	2	Q51T00_9CALI	Q51t00 notovitus s
317	16	22.2	14	2	Q7RBZ5_PLAYO	Q7rbz5 plasmodium	390	15	20.8	12	2	Q767J2_ONCKE	Q767j2 oncorhynch
318	16	22.2	14	2	P82332_PEA	P82332 pisum sativ	391	15	20.8	13	1	FLET_LIMPT	P82064 limodrymast
319	16	22.2	14	2	Q71IZ6_LACPL	Q71iz6 lacobocall	392	15	20.8	13	1	GRA2B_POCPU	P69843 pogonoperca
320	16	22.2	14	2	Q8VU21_STRPN	Q8vu21 streptococc	393	15	20.8	13	1	GRA2B_POCPU	P69844 pogonoperca
321	16	22.2	14	2	Q9R782_BACCI	Q9r782 bacillus il	394	15	20.8	13	1	GRAB_GRASK	P69841 grammitis
322	16	22.2	14	2	Q2MHR3_ECOLI	Q2mhr3 escherichia	395	15	20.8	13	1	TE1BA_RANBO	P84116 rana boylii
323	16	22.2	14	2	Q73591_CHICK	Q73591 gallus gall	396	15	20.8	13	1	TEML_RANTE	P57104 rana tempor

397	15	20.8	13	2	Q5H8A9_HUMAN	Q5H8a9 homo sapien	470	14	19.4	8	1	PPK2_BERAM	P82692 periplaneta
398	15	20.8	13	2	Q7IUN9_HUMAN	Q7Iun9 homo sapien	471	14	19.4	8	1	RS1_ERWCH	P37985 erwina chr
399	15	20.8	13	2	Q7M4I9_GIALA	Q7M4i9 giardia lam	472	14	19.4	8	2	Q15895_HUMAN	P13955 erwina chr
400	15	20.8	13	2	Q7RPA9_PLAYO	Q7RPa9 plasmodium	473	14	19.4	8	2	Q9POK3_HUMAN	Q9POK3 homo sapien
401	15	20.8	13	2	Q9J5U3_GRYTP	Q9J5u3 trypanosoma	474	14	19.4	8	2	Q9TW6_GAVNE	Q9TW6 periteneis
402	15	20.8	13	2	Q7M373_BOVIN	Q7M373 bos taurus	475	14	19.4	8	2	Q5W4V6_VIVRU	Q5W4V6 bacterioph
403	15	20.8	13	2	Q7YRD1_BISBO	Q7YRD1 bison bonas	476	14	19.4	8	2	Q5W4V6_9CAUD	Q5W4V6 bacterioph
404	15	20.8	13	2	Q7YRI4_BOVIN	Q7YRI4 bos taurus	477	14	19.4	8	2	Q5W4V8_BPE51	Q5W4V8 bacterioph
405	15	20.8	13	2	Q9TUD7_BOVIN	Q9TUD7 bos taurus	478	14	19.4	8	2	Q5W4W1_9CAUD	Q5W4W1 bacterioph
406	15	20.8	13	2	Q56YV8_ARATH	Q56YV8 arabidopsis	479	14	19.4	8	2	Q5W4W2_BPR32	Q5W4W2 bacterioph
407	15	20.8	13	2	Q8WEJ9_GINBI	Q8WEJ9 ginkgo bilo	480	14	19.4	8	2	Q5W4M4_9CAUD	Q5W4M4 bacterioph
408	15	20.8	13	2	Q945C1_CRYCO	Q945C1 cryptocodi	481	14	19.4	8	2	Q5W4W6_VIVRU	Q5W4W6 bacterioph
409	15	20.8	13	2	Q9GCU6_9LILI	Q9GCU6 veitchia ar	482	14	19.4	8	2	Q5W4X0_9CAUD	Q5W4X0 bacterioph
410	15	20.8	13	2	Q7M1A2_BACNO	Q7M1A2 bacteroides	483	14	19.4	8	2	Q5W4X2_9VIRU	Q5W4X2 bacterioph
411	15	20.8	13	2	Q9KHJ4_CAUCR	Q9KHJ4 caulobacter	484	14	19.4	8	2	Q5W4X4_9VIRU	Q5W4X4 bacterioph
412	15	20.8	13	2	Q7BEH3_MOUSE	Q7BEH3 mus musculi	485	14	19.4	8	2	Q5W4X6_BPJZ5	Q5W4X6 bacterioph
413	15	20.8	13	2	Q2WD52_FICHP	Q2WD52 ficedula hy	486	14	19.4	8	2	Q5W4X8_BPLZ4	Q5W4X8 bacterioph
414	15	20.8	13	2	Q2WD53_FICPA	Q2WD53 ficedula pa	487	14	19.4	8	2	Q5W4Y0_BPLZ1	Q5W4Y0 bacterioph
415	15	20.8	13	2	Q2WD61_FICAL	Q2WD61 ficedula al	488	14	19.4	8	2	Q5W4Y2_9CAUD	Q5W4Y2 bacterioph
416	15	20.8	13	1	ECDL_LYMDI	P80940 lymphotria d	489	14	19.4	8	2	Q5W4Y4_9CAUD	Q5W4Y4 bacterioph
417	15	20.8	14	1	MAST_VESOR	P17238 vespa orient	490	14	19.4	8	2	Q5W4Y6_BPR70	Q5W4Y6 bacterioph
418	15	20.8	14	2	Q50845_METVO	Q50845 methanococc	491	14	19.4	8	2	Q8H9H3_9CAUD	Q8H9H3 bacterioph
419	15	20.8	14	2	Q7S2V7_NEUCR	Q7S2V7 neurospora	492	14	19.4	8	2	Q8H9H5_BP16	Q8H9H5 bacterioph
420	15	20.8	14	2	Q9P2A2_HUMAN	Q9P2A2 homo sapien	493	14	19.4	8	2	Q8H9H6_BP17	Q8H9H6 bacterioph
421	15	20.8	14	2	Q5WQZ8_OPICA	Q5WQZ8 opisthoptha	494	14	19.4	8	2	Q8H9I2_BPR27	Q8H9I2 bacterioph
422	15	20.8	14	2	Q7RKW6_PLAYO	Q7RKW6 plasmodium	495	14	19.4	8	2	Q8H9I3_BPR27	Q8H9I3 bacterioph
423	15	20.8	14	2	Q85CA2_STRYDR	Q85CA2 strongyloce	496	14	19.4	8	2	Q8H9I4_9CAUD	Q8H9I4 bacterioph
424	15	20.8	14	2	Q85I00_9ECHO	Q85I00 anthrenoid	497	14	19.4	8	2	Q8H9I6_BPR15	Q8H9I6 bacterioph
425	15	20.8	14	2	Q7IGJ1_9HYME	Q7IGJ1 arbididopsis	498	14	19.4	8	2	Q8H9I8_9CAUD	Q8H9I8 bacterioph
426	15	20.8	14	2	Q9SMV4_ARATH	Q9SMV4 arbididopsis	499	14	19.4	8	2	Q8H9I9_BPR10	Q8H9I9 bacterioph
427	15	20.8	14	2	Q9R5I8_VIBAL	Q9R5I8 viorlio algi	500	14	19.4	8	2	Q8H9J1_BPR06	Q8H9J1 bacterioph
428	15	20.8	14	2	Q66IE1_BORGA	Q66IE1 borrella ga	501	14	19.4	8	2	Q8H9J3_BPR03	Q8H9J3 bacterioph
429	15	20.8	14	2	Q9ZOG5_MOUSE	Q9ZOG5 mus musculi	502	14	19.4	8	2	Q8H9J5_9CAUD	Q8H9J5 bacterioph
430	15	20.8	14	2	Q6JTU7_ONCMY	Q6JTU7 oncorhynch	503	14	19.4	8	2	Q8H9J7_BPR0X2	Q8H9J7 bacterioph
431	15	20.8	14	2	Q2OF76_MEIGA	Q2OF76 melagris g	504	14	19.4	8	2	Q8H9J9_BPR1	Q8H9J9 bacterioph
432	15	20.8	14	2	Q10Z34_9HIV1	Q10Z34 human immun	505	14	19.4	8	2	Q8H9K4_BPR3	Q8H9K4 bacterioph
433	15	20.8	15	1	APFL_MALPA	P83141 malva parvi	506	14	19.4	8	2	Q5DOK1_9LILI	Q5DOK1 locococcus
434	15	20.8	15	1	MCPI6_LYCES	P80812 lycopersico	507	14	19.4	8	2	Q5DOK8_9LILI	Q5DOK8 hyaristaele
435	15	20.8	15	1	Q4W378_GLECA	P22948 methanosarc	508	14	19.4	8	2	Q5DOK7_9LILI	Q5DOK7 gnilubia cos
436	15	20.8	15	2	Q4W378_GLECA	Q4W378 neurospogon	509	14	19.4	8	2	Q5DOK2_9LILI	Q5DOK2 gironophyllu
437	15	20.8	15	2	Q7M4Y5_FUSSP	Q7M4Y5 fusarium sp	510	14	19.4	8	2	Q5DOK9_9LILI	Q5DOK9 cythosperma
438	15	20.8	15	2	Q13377_HUMAN	Q13377 homo sapien	511	14	19.4	8	2	Q5DOP5_9LILI	Q5DOP5 clostridium
439	15	20.8	15	2	Q4X8U7_PLACH	Q4X8U7 plasmodium	512	14	19.4	8	2	Q45889_CLOBO	Q45889 borrella bu
440	15	20.8	15	2	Q4Y6J1_PLABE	Q4Y6J1 crassostrea	513	14	19.4	8	2	Q9R4M3_BMPRA	Q9R4M3 enterococcu
441	15	20.8	15	2	Q5K6Q7_CRAGI	Q5K6Q7 bemisia arg	514	14	19.4	8	2	Q8GJ21_BORBU	Q8GJ21 borrella bu
442	15	20.8	15	2	Q6JCR8_9HEMI	Q6JCR8 vulpes vulp	515	14	19.4	8	2	FARS_BENNO	P80975 penaeus mon
443	15	20.8	15	2	Q7M3B5_VULVU	Q7M3B5 oryctolagus	516	14	19.4	9	1	FLAA2_TREHY	P80320 treponema h
444	15	20.8	15	2	Q9RR8_RABIT	Q9RR8 arabidopsis	517	14	19.4	9	1	Q7RYB8_NEUCR	Q7RYB8 neurospora
445	15	20.8	15	2	Q42223_ARATH	Q42223 justicia am	518	14	19.4	9	1	Q7YR82_PLAYO	Q7YR82 diosiphila
446	15	20.8	15	2	Q4PZV5_JUSAM	Q4PZV5 rosmarinus	519	14	19.4	9	1	Q5ZES4_BOVIN	Q5ZES4 bos taurus
447	15	20.8	15	2	Q7OY59_ROSOF	Q7OY59 chlamydomon	520	14	19.4	9	2	Q8HZY2_CANPA	Q8HZY2 canis famli
448	15	20.8	15	2	Q8SLJ6_9MAGN	Q8SLJ6 mycobacteti	521	14	19.4	9	2	Q8TUYO_MONDO	Q8TUYO monodelphis
449	15	20.8	15	2	Q9T202_CHLRE	Q9T202 mus musculi	522	14	19.4	9	2	Q5DOK7_9LILI	Q5DOK7 nega punil
450	15	20.8	15	2	Q9R544_MYCBO	Q9R544 mesocricetu	523	14	19.4	9	2	Q5DOK6_9LILI	Q5DOK6 hyaristaele
451	15	20.8	15	2	Q19468_MOUSE	Q19468 mus musculi	524	14	19.4	9	2	Q5DOK8_9LILI	Q5DOK8 gironophyllu
452	15	20.8	15	2	Q8B175_MOUSE	Q8B175 mus musculi	525	14	19.4	9	2	Q5DOK9_9LILI	Q5DOK9 gironophyllu
453	15	20.8	15	2	Q3MUG6_MESAU	Q3MUG6 mus sp. 16	526	14	19.4	9	2	Q5DOK4_9LILI	Q5DOK4 areca rheop
454	15	20.8	15	2	Q9QV01_9MURI	Q9QV01 rattus sp.	527	14	19.4	9	2	Q5DOK1_9LILI	Q5DOK1 manictaria s
455	15	20.8	15	2	Q9QV17_9MURI	Q9QV17 rattus sp.	528	14	19.4	9	2	Q7OY83_9LAMI	Q7OY83 leopoldinia
456	15	20.8	15	2	Q9QVNO_9MURI	Q9QVNO oncorhynch	529	14	19.4	9	2	Q5DOP2_9LILI	Q5DOP2 kentilopsis
457	15	20.8	15	2	P83333_ONCMY	P83333 gallus galli	530	14	19.4	9	2	Q5DOP3_9LILI	Q5DOP3 ignanura wa
458	15	20.8	15	2	Q7ILZ20_CHICK	Q7ILZ20 gallus amerc	531	14	19.4	9	2	Q5DOP4_9LILI	Q5DOP4 amandara de
459	15	20.8	15	2	Q9TH04_GRUAM	Q9TH04 cydia pomon	532	14	19.4	9	2	Q8GLZ6_BORBU	Q8GLZ6 borrella bu
460	15	20.8	12	2	Q9TRU9_BOVIN	Q9TRU9 bos taurus	533	14	19.4	9	2		
461	14.5	20.1	12	2	PPH2_LYCES	PPH2 lycopersico	534	14	19.4	9	2		
462	14	19.4	7	1	UNO6_PIPNS	UNO6 pinus pinas	535	14	19.4	9	2		
463	14	19.4	7	1	Q15903_HUMAN	Q15903 homo sapien	536	14	19.4	9	2		
464	14	19.4	7	2	Q8GL04_BORBU	Q8GL04 borrella bu	537	14	19.4	9	2		
465	14	19.4	8	1	ALLI5_CARMA	P81819 carcinus ma	538	14	19.4	9	2		
466	14	19.4	8	1	ALLI6_CARMA	P81818 carcinus ma	539	14	19.4	9	2		
467	14	19.4	8	1	ALL3_CYDPO	P82155 cydia pomon	540	14	19.4	9	2		
468	14	19.4	8	1	ALL4_CAYVO	P82155 cydia pomon	541	14	19.4	9	2		
469	14	19.4	8	1	ALL4_CYDPO	P82155 cydia pomon	542	14	19.4	9	2		

543	14	19.4	9	2	Q9R3C4	BORBU	Q9r9c4	borrella bu	616	14	19.4	12	2	Q673J1	PANPA	Q673j1	pan paniscu
544	14	19.4	9	2	Q3TMU8	MOUSE	Q3tm8	mus musculus	617	14	19.4	12	2	Q673J2	PANTR	Q673j2	pan troglod
545	14	19.4	9	2	Q4MBQ9	MOUSE	Q4mb9	mus musculus	618	14	19.4	12	2	Q9T2U3	BOVIN	Q9t2u3	bos taurus
546	14	19.4	9	2	Q6YF34	RAT	Q6yf34	rattus norv	619	14	19.4	12	2	Q9TRY4	GCETA	Q9try4	sus sp. ins
547	14	19.4	9	2	Q9QZ47	MOUSE	Q9qz47	mus musculus	620	14	19.4	12	2	P940I1	ARATH	P940i1	arabidopsis
548	14	19.4	9	2	Q8JFA6	FICHY	Q8jfa6	ficedula hy	621	14	19.4	12	2	Q2T180	SOYBN	Q2t180	glycine max
549	14	19.4	10	1	Q8JFA7	FICLAL	Q8jfa7	ficedula al	622	14	19.4	12	2	Q41856	MAIZE	Q41856	zea mays (m
550	14	19.4	10	1	COX81	SHEEP	P803j7	ovis aries	623	14	19.4	12	2	Q5DQK4	GLILI	Q5dqk4	hydrastele
551	14	19.4	10	1	MBSP	SAUWA	P844r6	sauida wan	624	14	19.4	12	2	Q5DQJ5	GLILI	Q5dqj5	hydrastele
552	14	19.4	10	1	SC64	TITCA	P845r2	citrus camb	625	14	19.4	12	2	Q5DQJ3	GLILI	Q5dqj3	gultibia cos
553	14	19.4	10	1	TEBK	RANTE	P569r3	rana tempor	626	14	19.4	12	2	Q5DQJ1	GLILI	Q5dqj1	gromophyllu
554	14	19.4	10	1	UHA3	HUMAN	P409r0	homo sapien	627	14	19.4	12	2	Q5KSP0	SYMFO	Q5ksp0	sympllocarpu
555	14	19.4	10	2	Q7S225	NEUCR	Q7s225	neurospora	628	14	19.4	12	2	Q7MIU3	ORYSA	Q7miu3	oryza sativ
556	14	19.4	10	2	Q7S2K0	NEUCR	Q7s2k0	neurospora	629	14	19.4	12	2	Q7M2G3	VICPA	Q7m2g3	vicena faba
557	14	19.4	10	2	Q7LDT7	HUMAN	Q7ldt7	homo sapien	630	14	19.4	12	2	Q9PSA9	GCARY	Q9psa9	silene aega
558	14	19.4	10	2	Q4X4H2	PLACH	Q4x4h2	plasmodium	631	14	19.4	12	2	Q5DON7	GLILI	Q5don7	socratea ex
559	14	19.4	10	2	Q4X6X5	PLACH	Q4x6x5	plasmodium	632	14	19.4	12	2	Q500I9	MYCLE	Q500i9	mycobacteri
560	14	19.4	10	2	Q7M4C9	HEMPU	Q7m4c9	hemientrot	633	14	19.4	12	2	Q83U71	SALET	Q83u71	salmonella
561	14	19.4	10	2	Q7M4D8	ANTCR	Q7m4d8	anthocidari	634	14	19.4	12	2	Q9S4K7	ECOLI	Q9s4k7	escherichia
562	14	19.4	10	2	Q7M2U1	BOVIN	Q7m2u1	bos taurus	635	14	19.4	12	2	Q9X636	KLB0X	Q9x636	klebsiella
563	14	19.4	10	2	Q67B26	9CAUD	Q67b26	bacterioph	636	14	19.4	12	2	Q3TRQ3	MOUSE	Q3trq3	mus musculus
564	14	19.4	10	2	Q5DQJ5	GLILI	Q5dqj5	siphkentia	637	14	19.4	12	2	Q2Q8P5	PHYFS	Q2q8p5	phyllioscopu
565	14	19.4	10	2	Q5DQJ6	GLILI	Q5dqj6	pinanga cor	638	14	19.4	12	2	Q2Q8P6	PHYBO	Q2q8p6	phyllioscopu
566	14	19.4	10	2	Q5DQK0	GLILI	Q5dqk0	loxococcus	639	14	19.4	12	2	Q2Q8P7	PHYSI	Q2q8p7	phyllioscopu
567	14	19.4	10	2	Q5DQMO	GLILI	Q5dqmo	gultibia lon	640	14	19.4	12	2	Q2Q8P8	PHYTO	Q2q8p8	phyllioscopu
568	14	19.4	10	2	Q5DQJ5	GLILI	Q5dqj5	gromophyllu	641	14	19.4	12	2	Q2Q8P9	PHYTO	Q2q8p9	phyllioscopu
569	14	19.4	10	2	Q5DQJ5	GLILI	Q5dqj5	gromophyllu	642	14	19.4	12	2	Q2Q8Q0	PHYCO	Q2q8q0	phyllioscopu
570	14	19.4	10	2	Q5DQJ8	GLILI	Q5dqj8	reinhardtia	643	14	19.4	12	2	Q2Q8Q2	PHYCO	Q2q8q2	phyllioscopu
571	14	19.4	10	2	Q5DQJ0	GLILI	Q5dqj0	normalhya n	644	14	19.4	12	2	Q2Q8Q3	PHYBE	Q2q8q3	phyllioscopu
572	14	19.4	10	2	Q85V66	EUCAR	Q85v66	eucalyptus	645	14	19.4	12	2	Q2Q8R6	PHYTC	Q2q8r6	phyllioscopu
573	14	19.4	10	2	Q9FS93	GCARY	Q9fs93	silene pent	646	14	19.4	12	2	Q5ERY2	GHIVI	Q5ery2	human immun
574	14	19.4	10	2	Q5DQJ5	GLILI	Q5dqj5	areca conc	647	14	19.4	12	2	Q5ERY2	GHIVI	Q5ery2	human immun
575	14	19.4	10	2	Q5DQJ2	GLILI	Q5dqj2	hydrastele	648	14	19.4	12	2	Q5ERY2	GHIVI	Q5ery2	human immun
576	14	19.4	10	2	Q52837	RHILE	Q52837	rhizobium l	649	14	19.4	12	2	Q5ERY2	GHIVI	Q5ery2	human immun
577	14	19.4	10	2	Q5D4Q3	GRHO	Q5d4q3	azospira or	650	14	19.4	12	2	Q5ERY2	GHIVI	Q5ery2	human immun
578	14	19.4	10	2	Q5D4Q4	GRHO	Q5d4q4	dechloromon	651	14	19.4	12	2	Q5EUV0	GHIVI	Q5euvo	human immun
579	14	19.4	10	2	Q9JN49	STRAU	Q9j49	staphylococ	652	14	19.4	12	2	Q5EUV2	GHIVI	Q5eu2	human immun
580	14	19.4	10	2	Q9LSM6	LIBAC	Q9lsm6	liberibacte	653	14	19.4	12	2	Q5EUV10	GHIVI	Q5eu10	human immun
581	14	19.4	10	2	Q8G8W5	BORBU	Q8g8w5	borrella bu	654	14	19.4	12	2	Q5EUV12	GHIVI	Q5eu12	human immun
582	14	19.4	10	2	Q9JL15	MOUSE	Q9jl15	mus musculu	655	14	19.4	12	2	Q5EUV20	GHIVI	Q5eu20	human immun
583	14	19.4	10	2	Q2WDB9	FICLAL	Q2wdb9	ficedula al	656	14	19.4	12	2	Q5EUV22	GHIVI	Q5eu22	human immun
584	14	19.4	10	2	Q9PRY8	TRISC	Q9pry8	trilakis scy	657	14	19.4	12	2	Q5EUV24	GHIVI	Q5eu24	human immun
585	14	19.4	11	1	BR3	MEGFL	P12797	megascollia	658	14	19.4	12	2	Q900D1	GHIVI	Q900d1	human immun
586	14	19.4	11	1	RS30	ONCMY	P833z8	oncorhynch	659	14	19.4	12	2	Q9ICES	GHIVI	Q9ices	human immun
587	14	19.4	11	2	Q9UR95	PICAN	Q9ur95	pichia angu	660	14	19.4	13	1	TEICA	RANCL	TEICA	oryza sativ
588	14	19.4	11	2	Q9URP5	HUMAN	Q9urp5	homo sapien	661	14	19.4	13	1	TEICD	RANCL	TEICD	oryza ciamic
589	14	19.4	11	2	Q4X8K4	PLACH	Q4x8k4	plasmodium	662	14	19.4	13	1	TEICE	RANCL	TEICE	rana ciamic
590	14	19.4	11	2	Q4YD43	PLABE	Q4yd43	plasmodium	663	14	19.4	13	1	TEILA	RANLU	TEILA	rana luteiv
591	14	19.4	11	2	Q6LC30	FASHE	Q6lc30	fasciola he	664	14	19.4	13	2	Q7M4Y6	FUSSP	Q7m4y6	methanococc
592	14	19.4	11	2	Q7RH63	PLAYO	Q7rh63	plasmodium	665	14	19.4	13	2	Q508J1	METVO	Q508j1	leptomonas
593	14	19.4	11	2	Q4SX12	9EUTH	Q4sx12	zebra mays (m	666	14	19.4	13	2	Q2TIL5	GLILI	Q2til5	gultibia cy1
594	14	19.4	11	2	Q6JDK6	CANFA	Q6jdk6	canis famli	667	14	19.4	13	2	Q8WYB7	HUMAN	Q8wyb7	homo sapien
595	14	19.4	11	2	Q7M374	BOVIN	Q7m374	bos taurus	668	14	19.4	13	2	Q9UM84	HUMAN	Q9um84	homo sapien
596	14	19.4	11	2	Q9TQSO	BOVIN	Q9tqso	bos taurus	669	14	19.4	13	2	Q4QVZ6	9BIVA	Q4qvz6	cridaena gi
597	14	19.4	11	2	Q5DQJ6	GLILI	Q5dqj6	hydrastele	670	14	19.4	13	2	Q50L81	9DIPR	Q50l81	drosophila
598	14	19.4	11	2	Q5DQJ8	GLILI	Q5dqj8	gultibia pal	671	14	19.4	13	2	Q6SEB0	DROSI	Q6seb0	drosophila
599	14	19.4	11	2	Q7X9Y3	CUCSA	Q7x9y3	cucumis sat	672	14	19.4	13	2	Q812E2	PLAF7	Q812e2	plasmodium
600	14	19.4	11	2	Q8RY30	MAIZE	Q8ry30	zea mays (m	673	14	19.4	13	2	Q9ARE2	LEPSE	Q9are2	leptomonas
601	14	19.4	11	2	Q44237	9NOST	Q44237	anabaena sp	674	14	19.4	13	2	Q2TIL5	GLILI	Q2til5	gultibia cy1
602	14	19.4	11	2	Q8GL19	BORBU	Q8gl19	borrella bu	675	14	19.4	13	2	Q5DQJ3	GLILI	Q5dqj3	hydrastele
603	14	19.4	11	2	Q8GL24	BORBU	Q8gl24	borrella bu	676	14	19.4	13	2	Q5DQJ9	GLILI	Q5dqj9	gultibia mac
604	14	19.4	11	2	Q61797	MOUSE	Q61797	mus musculu	677	14	19.4	13	2	Q5DQJ4	GLILI	Q5dqj4	gromophyllu
605	14	19.4	11	2	Q6RZ06	ONCMY	Q6rz06	oncorhynch	678	14	19.4	13	2	Q7DMV2	ACTUDE	Q7dmv2	actinidia d
606	14	19.4	11	2	Q85620	MUWMO	Q85620	moloney mut	679	14	19.4	13	2	Q9FS94	GCARY	Q9fs94	silene pent
607	14	19.4	12	1	P4R7	PENMO	P833z2	penaeus mon	680	14	19.4	13	2	Q9FSAB	SILBA	Q9fsab	silene bacc
608	14	19.4	12	2	Q16405	HUMAN	Q16405	homo sapien	681	14	19.4	13	2	Q798K6	STREP	Q798k6	streplococc
609	14	19.4	12	2	Q4XWZ8	PLACH	Q4xwz8	plasmodium	682	14	19.4	13	2	Q9R8R9	STRPY	Q9r8r9	streplococc
610	14	19.4	12	2	Q8T0Y6	APIME	Q8t0y6	apis mellif	683	14	19.4	13	2	Q9XBY0	9BACT	Q9xb0	nitrogen-fi
611	14	19.4	12	2	Q9TWV4	LYNST	Q9twv4	lymaea sta	684	14	19.4	13	2	Q47607	ECOLI	Q47607	escherichia
612	14	19.4	12	2	Q673I4	PAPCY	Q673i4	papio cynoc	685	14	19.4	13	2	Q9R3R3	BORBU	Q9r3r3	borrella bu
613	14	19.4	12	2	Q673I5	PAPPA	Q673i5	papio papio	686	14	19.4	13	2	Q8B5N4	9BACU	Q8b5n4	epinotia ap
614	14	19.4	12	2	Q673I7	PONPY	Q673i7	pongo pygma	687	14	19.4	13	2	Q2Q8P4	PHYFS	Q2q8p4	phyllioscopu
615	14	19.4	12	2	Q673I9	9PRIM	Q673i9	gorilla gor	688	14	19.4	13	2	Q2WDT0	FICHY	Q2wdt0	ficedula hy

689	14	19.4	13	2	Q2WDT1_FICPA	Q2wdt1 ficedula pa
690	14	19.4	13	2	Q2WDT8_FICAL	Q2wdt8 ficedula al
691	14	19.4	13	2	Q6W746_9RETR	Q6w746 equine infe
692	14	19.4	13	2	Q86327_9RETR	Q86327 rous sarcom
693	14	19.4	13	2	Q86328_9RETR	Q86328 rous sarcom
694	14	19.4	14	1	COCO_LIMPO	P35586 ltimulub pol
695	14	19.4	14	1	CWP09_LYCES	P80806 lycopersico
696	14	19.4	14	1	GLPK_STYRCS	P25013 streptomyce
697	14	19.4	14	1	HLP1_HYLPV	P84922 hyia puncia
698	14	19.4	14	1	MAST_VESBA	P21654 vespa basai
699	14	19.4	14	1	MAST_VESLE	P01514 vespuia lew
700	14	19.4	14	1	MAST_VESMA	P04205 vespa manda
701	14	19.4	14	1	MAST_VESSA	P04105 vespa xanth
702	14	19.4	14	1	MCRZ_METTM	P58816 methanobact
703	14	19.4	14	1	RS19_PPMBP	P52093 pigeon pea
704	14	19.4	14	1	TEILB_RANLU	P82831 rana luteiv
705	14	19.4	14	1	Q2KGV1_MAGGR	Q2kqv1 magnaporthe
706	14	19.4	14	2	Q93057_HUMAN	Q93057 homo sapien
707	14	19.4	14	2	Q9P0K5_HUMAN	Q9p0k5 homo sapien
708	14	19.4	14	2	P82209_BOMMO	P82209 bombyx mori
709	14	19.4	14	2	Q50L76_DROAN	Q50l76 drosophila
710	14	19.4	14	2	Q7REF3_PLAYO	Q7ref3 plasmodium
711	14	19.4	14	2	Q9G3C0_9DIPT	Q9g3c0 calliphora
712	14	19.4	14	2	Q7JGT8_9HYME	Q7jgt8 andrena dto
713	14	19.4	14	2	Q7M385_PIG	Q7m385 sus scrofa
714	14	19.4	14	2	Q8HYM2_FELCA	Q8hym2 felis silve
715	14	19.4	14	2	Q9TRR83_PIG	Q9trr83 sus scrofa
716	14	19.4	14	2	Q67B14_9CAUD	Q67b14 bacterioph
717	14	19.4	14	2	P84491_CUCMA	P84491 cucurbita m
718	14	19.4	14	2	Q5DOK_9LILI	Q5dok9 hydrataetele
719	14	19.4	14	2	Q5DOL_9LILI	Q5dol10 hydrataetele
720	14	19.4	14	2	Q5DQL_9LILI	Q5dql10 hydrataetele
721	14	19.4	14	2	Q5DQNL_9LILI	Q5dqnl7 gulubia sp.
722	14	19.4	14	2	Q5DQNL_9LILI	Q5dqnl9 ptychoperm
723	14	19.4	14	2	Q7M1G6_AYVSA	Q7m1g6 avena sativ
724	14	19.4	14	2	Q9FS91_9CARY	Q9fs91 silene sedo
725	14	19.4	14	2	Q9FS95_9CARY	Q9fs95 silene pent
726	14	19.4	14	2	Q9FSB1_9CARY	Q9fsb1 silene aega
727	14	19.4	14	2	Q9LEH4_HORVU	Q9leh4 hordeum vul
728	14	19.4	14	2	Q45872_CLOBO	Q45872 clostridium
729	14	19.4	14	2	Q9R225_CAMJE	Q9r225 campylobact
730	14	19.4	14	2	Q9W79_9CAMCO	Q9w79 campylobact
731	14	19.4	14	2	Q9ZB42_STRPY	Q9zb42 streptococc
732	14	19.4	14	2	Q9PMT9_CAMJE	Q9pmt9 campylobact
733	14	19.4	14	2	P70319_MOUSE	P70319 mus musculu
734	14	19.4	14	2	Q7M058_MOUSE	Q7m058 mus musculu
735	14	19.4	14	2	P70007_XENLIA	P70007 xenopus lae
736	14	19.4	14	2	Q20801_PHYCO	Q20801 phylococcu
737	14	19.4	14	2	Q208R4_PHYTC	Q208r4 phylococcu
738	14	19.4	15	1	ACPE_WHEAT	P83184 trititulum ae
739	14	19.4	15	1	CWP28_LYCES	P80824 lycopersico
740	14	19.4	15	1	FGF1_CANFA	P16651 canis famli
741	14	19.4	15	1	MPAO2_ORYSA	P83466 oryza sativ
742	14	19.4	15	1	RIJ1_STRAU	O94520 streptomyce
743	14	19.4	15	2	Q9TW63_THRELI	Q9tw63 thermococcu
744	14	19.4	15	2	Q9UWH3_THRELI	Q9uwh3 thermococcu
745	14	19.4	15	2	Q7M4X6_FUSSP	Q7m4x6 fusarium sp
746	14	19.4	15	2	Q7M4Y8_FUSSP	Q7m4y8 fusarium sp
747	14	19.4	15	2	Q7S459_NEUCR	Q7s459 neurospora
748	14	19.4	15	2	Q7SH11_NEUCR	Q7sh11 neurospora
749	14	19.4	15	2	Q9UR64_PLEOS	Q9ur64 pleurotus o
750	14	19.4	15	2	Q9UR72_TRIHA	Q9ur72 trichodetma
751	14	19.4	15	2	Q16158_HUMAN	Q16158 homo sapien
752	14	19.4	15	2	Q6LC13_HUMAN	Q6lc13 homo sapien
753	14	19.4	15	2	Q6TARI_HUMAN	Q6tari homo sapien
754	14	19.4	15	2	Q7M4R1_HUMAN	Q7m4r1 homo sapien
755	14	19.4	15	2	Q7M4S6_HUMAN	Q7m4s6 homo sapien
756	14	19.4	15	2	Q66VY8_HUMAN	Q66vy8 homo sapien
757	14	19.4	15	2	Q8TC57_HUMAN	Q8tc57 homo sapien
758	14	19.4	15	2	Q9TNP2_HUMAN	Q9tnp2 homo sapien
759	14	19.4	15	2	Q9UCB9_HUMAN	Q9ucb9 homo sapien
760	14	19.4	15	2	Q9UCV8_HUMAN	Q9ucv8 homo sapien
761	14	19.4	15	2	Q4XQUS_PLACH	Q4xqus plasmodium

762	14	19.4	15	2	Q4YF12_PLABE	Q4yf12 plasmodium
763	14	19.4	15	2	Q4YUB4_PLABE	Q4yub4 plasmodium
764	14	19.4	15	2	Q6SLH8_CAEEL	Q6slh8 caenorhabd
765	14	19.4	15	2	Q7R6M8_PLAYO	Q7r6m8 plasmodium
766	14	19.4	15	2	Q9TW5_9CUS	Q9tw5 attemia (br
767	14	19.4	15	2	Q7IGM2_9HYME	Q7igm2 andrena n.
768	14	19.4	15	2	Q71GV6_9HYME	Q71gv6 andrena sim
769	14	19.4	15	2	Q71H38_9HYME	Q71h38 andrena aur
770	14	19.4	15	2	Q4G3Y8_MACMU	Q4g3y8 macaca mula
771	14	19.4	15	2	Q9TQO5_BOVIN	Q9tqo5 bos taurus
772	14	19.4	15	2	Q5DQML_9LILI	Q5dqml gulubia lon
773	14	19.4	15	2	Q6Z263_9CARY	Q6z263 silene nigr
774	14	19.4	15	2	Q6Z274_9CARY	Q6z274 lycnis flo
775	14	19.4	15	2	Q6Z276_LYCH	Q6z276 lycnis cha
776	14	19.4	15	2	Q6Z277_9CARY	Q6z277 silene coel
777	14	19.4	15	2	Q7DLP1_SOLUTU	Q7dlp1 solanum tub
778	14	19.4	15	2	Q7M1S8_ORYSA	Q7m1s8 oryza sativ
779	14	19.4	15	2	Q9FEI3_9CARY	Q9fei3 silene aega
780	14	19.4	15	2	Q9FEI4_9CARY	Q9fei4 silene pent
781	14	19.4	15	2	Q9FEI5_9CARY	Q9fei5 silene sedo
782	14	19.4	15	2	Q9FS80_9CARY	Q9fs80 silene zava
783	14	19.4	15	2	Q9FS98_9CARY	Q9fs98 silene iaco
784	14	19.4	15	2	Q9FS99_9CARY	Q9fs99 silene inte
785	14	19.4	15	2	Q9FSA0_9CARY	Q9fsa0 silene haus
786	14	19.4	15	2	Q9FSB0_9CARY	Q9fsb0 silene cryp
787	14	19.4	15	2	Q9FSB2_9CARY	Q9fsb2 silene aega
788	14	19.4	15	2	Q9SAP4_SOLUTU	Q9sap4 solanum tub
789	14	19.4	15	2	Q9TRK8_SPIOL	Q9trk8 spinacia ol
790	14	19.4	15	2	Q3IXN5_SHIBS	Q3ixn5 shigella bo
791	14	19.4	15	2	Q3IYYP_SHISS	Q3iyye shigella so
792	14	19.4	15	2	Q46013_CAVCR	Q46013 callobacter
793	14	19.4	15	2	Q8X2E0_ECO57	Q8x2e0 escherichia
794	14	19.4	15	2	Q9R4D6_ECOLI	Q9r4d6 escherichia
795	14	19.4	15	2	Q9R4M6_BACFI	Q9r4m6 bacillus fi
796	14	19.4	15	2	Q9R533_PSEBA	Q9r534 pseudomonas
797	14	19.4	15	2	Q9R545_MYCBO	Q9r545 mycobacteri
798	14	19.4	15	2	Q9R548_MYCBO	Q9r548 mycobacteri
799	14	19.4	15	2	Q2MH50_ECOLI	Q2mhs0 escherichia
800	14	19.4	15	2		

ALIGNMENTS

RESULT 1

Q7M4W9_FLAVE PRELIMINARY; PRT; 14 AA.
 Q7M4W9,
 15-DEC-2003, integrated into UniProtKB/TrEMBL.

DT 15-DEC-2003, sequence version 1.
 DT 07-FEB-2006, entry version 6.
 DE Protein PFI3 (Fragment).

OS Flammulina velutipes.
 OC Basidiomycota; Basidiomycetes; Homobasidiomycetes;

OC Agaricales; Tricholomataceae; Flammulina.
 OX NCBI_TaxID=38945;
 RN [1]

RP PROTEIN SEQUENCE.
 RA Sakamoto Y., Ando A., Tamai Y., Miura K.;

RU Submitted (NOV-1999) to the PIR data bank.
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DR PIR: C59137; C59137.
 CC

FT NON_TER 1
 FT NON_TER 14

SQ SEQUENCE 14 AA; 1542 MW; 543980871D704053 CRC64;

Query Match 34.7%; Score 25; DB 2; Length 14;
 Best Local Similarity 66.7%; Pred. No. 3.8e+03;
 Matches 4; Conservative 2; Mismatches 0; Indels 0;

QY 1 VPFSVA 6
| | | | :
Db 9 VPFSIS 14

RESULT 2
Q798U8_STROR PRELIMINARY; PRT; 15 AA.

AC Q798U8_1
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 7.
DE Adenosine triphosphatase (EC 3.6.1.3) (Fragment).
GN Name-atpA;
OS Streptococcus oralis.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1303;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NCTC 11427;
RX MEDLINE=95020593; PubMed=7934882;
RA Renoll A., Munoz R., Garcia E., de la Campa A.G.;
RT Molecular basis of the optochin-sensitive phenotype of pneumococcus:
RT characterization of the genes encoding the F0 complex of the
RT Streptococcus pneumoniae and Streptococcus oralis H(+)-ATPases.";
RL Mol. Microbiol. 12:587-598(1994).

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CC
CC EMBL; Z26853; CAAB1457.1; -: Genomic DNA.
DR GO; GO:0042624; F:ATPase activity, uncoupled; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
KW Hydrolase.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1670 MW; 0ADE2A58DBD9D248 CRC64;

Query Match 33.3%; Score 24; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 6.3e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 9 VKSLYLIG 15
| | | | :
Db 1 LSSMYLG 7

RESULT 3
MDAR2_SOYBN STANDARD; PRT; 10 AA.

AC Q9S9Z6;
DT 19-JUL-2004, integrated into UniProtKB/Swiss-Prot.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Monodehydroascorbate reductase II (EC 1.6.5.4) (MDARII) (MRII)
DE (Ascorbate free radical reductase II) (AFR reductase II) (Fragment).
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Rosids; eustosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
OC Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP PROTEIN SEQUENCE, CATALYTIC ACTIVITY, AND COFACTOR.
RC STRAIN=cv. Williams; TISSUE=Root nodules;
RX MEDLINE=92088257; PubMed=1727643;
RA Dalton D.A., Langeberg L., Robbins M.;
RT Purification and characterization of monodehydroascorbate reductase
RT from soybean root nodules.";
RL Arch. Biochem. Biophys. 292:281-286(1992).

CC
CC -1- FUNCTION: Catalyzes the conversion of monodehydroascorbate to
CC ascorbate, oxidizing NADH in the process.
CC -1- CATALYTIC ACTIVITY: NADH + 2 monodehydroascorbate = NAD(+) + 2

CC ascorbate.
CC -1- COFACTOR: FAD.
CC -1- BIOPHYSICOCHEMICAL PROPERTIES:
CC Kinetic parameters:
CC KM=5.6 uM for NADH;
CC KM=150 uM for NADPH;
CC KM=7 uM for monodehydroascorbate;
CC Vmax=288 umol/min/mg enzyme for NADH oxidation reaction;
CC pH dependence:
CC Optimum pH is 8.0-9.0;

CC -1- SIMILARITY: Belongs to the FAD-dependent oxidoreductase family.
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CC
CC PIR; A44871; A44871.
KW Direct protein sequencing; FAD; Flavoprotein; NAD; Oxidoreductase;
KW Redox-active center.
FT CHAIN <1
FT NP_BIND 5 >10 Monodehydroascorbate reductase II.
FT NON_TER 1 1 /FTID=PRO_0000209144.
FT NON_TER 10 10 FAD (ADP part) (By similarity).
SQ SEQUENCE 10 AA; 1153 MW; 848025504B5339D1 CRC64;

Query Match 31.9%; Score 23; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 6.3e+03;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 AKSVKSLYLIG 15
| | | | :
Db 1 AKTFKYLIG 10

RESULT 4
CRBL_VESOR STANDARD; PRT; 14 AA.

AC P17236;
DT 01-AUG-1990, integrated into UniProtKB/Swiss-Prot.
DT 01-AUG-1990, sequence version 1.
DT 07-FEB-2006, entry version 31.
DE Histamine-releasing peptide 2 (Histamine-releasing peptide II) (HR-II).
OS Vespa orientalis (Oriental hornet).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespa.
OX NCBI_TaxID=7447;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Venom.
RA Miroschnikov A.I., Snezhkova L.G., Nazimov I.V., Reshetova O.I.,
RA Rozyunov B.V., Gushchin I.S.;
RT Structure and properties of histamine releasing peptides from the
RT venom of Vespa orientalis hornet.";
RL Bioorg. Khim. 7:1467-1477(1981).

CC -1- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis
CC of neutrophils.
CC -1- SUBCELLULAR LOCATION: Secreted protein.
CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -1- SIMILARITY: Belongs to the MCD family. Crabrolin subfamily.
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CC
CC PIR; JN0390; JN0390.
KW Amidation; Chemotaxis; Direct protein sequencing;
KW Mast cell degranulation; Sensory transduction.
FT PEPTIDE 1 14 /FTID=PRO_0000044048.
FT MOD_RES 14 14 Leucine amide.
SQ SEQUENCE 14 AA; 1524 MW; 22015B4A6CEPDF38 CRC64;

```

Query Match      31.9%; Score 23; DB 1; Length 14;
Best Local Similarity 41.7%; Pred. No. 9e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy
  1 VPSVAKSVKSL 12
    :|:|:|:|
    2 LPLILGKLKVL 13

RESULT 5
OSG1T6 ASPFL PRELIMINARY; PRT; 14 AA.
ID OSG1T6 ASPFL PRELIMINARY; PRT; 14 AA.
AC OSG1T6;
DT 01-MAR-2005, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE CyPA (Fragment).
GN Name=CyPA;
OS Aspergillus flavus.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5059;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AL 3-9, NC 5-2, and VA 4-4;
RX PubMed=16154781; DOI=10.1016/j.fgb.2005.07.004;
RA Chang P.K., Horn B.W., Dörner J.W.;
RT "Sequence breakpoints in the aflatoxin biosynthesis gene cluster and flanking regions in nonaflatoxinogenic Aspergillus flavus isolates.";
RL Fungal Genet. Biol. 42:914-923(2005).
[2]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=AL 3-9, NC 5-2, and VA 4-4;
RA Chang P.-K., Scharfenstein L.L.;
RT "Deletion of the aflatoxin gene cluster in Aspergillus flavus isolates.";
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AY864290; AAM58149.1; -; Genomic_DNA.
DR EMBL; AY864291; AAM58150.1; -; Genomic_DNA.
DR EMBL; AY864289; AAM58148.1; -; Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1432 MW; D875197AF5583D CRC64;

Query Match      31.9%; Score 23; DB 2; Length 14;
Best Local Similarity 45.5%; Pred. No. 9e+03;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy
  2 PFSVAKSVKSL 12
    ||:|:|:|
    2 PFTVRAKYTGL 12

RESULT 6
Q7M487 ANDAU PRELIMINARY; PRT; 14 AA.
ID Q7M487 ANDAU PRELIMINARY; PRT; 14 AA.
AC Q7M487;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Hemocyanin chain 3C (Fragment).
OS Androctonus australis (Sahara scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Butidae; Butioidae; Butidae; Androctonus.
OX NCBI_TaxID=6858;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=80047238; PubMed=499512; DOI=10.1016/0014-5793(79)80516-5;
RA Jolles J., Jolles P., Lamy J., Lamy J.;
RT "Structural characterization of seven different subunits in

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RT Androctonus australis haemocyanin.";
RL FEBS Lett. 106:289-291(1979).
CC -----
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CC -----
DR PIR; G61308; G61308.
FT NON_TER 1
FT NON_TER 14
SQ SEQUENCE 14 AA; 1670 MW; 7516B69D604114 CRC64;

Query Match      31.9%; Score 23; DB 2; Length 14;
Best Local Similarity 25.0%; Pred. No. 9e+03;
Matches 3; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy
  2 PFSVAKSVKSL 13
    |::|:|:|
    2 PINIQRIILSLF 13

RESULT 7
Q3TU57 MOUSE PRELIMINARY; PRT; 14 AA.
ID Q3TU57 MOUSE PRELIMINARY; PRT; 14 AA.
AC Q3TU57;
DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE 15 days embryo head cDNA, RIKEN full-length enriched library, full
DE clone:402414009 product:soybin and Sh3 domain containing 1, full
DE insert sequence. (Fragment).
GN Name=Soxbs1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carrinci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Methods Enzymol. 303:19-44(1999).
[2]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Carrinci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maida N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA Banal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chin K.P., Choudhary V., Christoflets A., Clutterbuck D.R.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagioli M., Paulner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Fukushima S., Gariboldi M.,
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA Gustincich S., Harbers M., Hayashizaki Y., Hensch T.K., Hirokawa N.,
RA Hill D., Hummichek L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA Kitano H., Koike S., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Mottagui-Tabar S., Mulder N., Nakano N., Nakaochi H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schonbach C., Sekiguchi K., Sempile C.A., Seno S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugita K., Sultana R., Takenaka Y., Taki K.,

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RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
 RA Ueda A.H., van Nimwegen E., Verardo R., Wei C.L., Yeai K.,
 RA Yamashita H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
 RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
 RA Mahlestedt C., Matick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 RA Fukuda S., Kanamori-Karayama M., Suzuki M., Aoki J., Arakawa T.,
 RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
 RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Niimomiya N.,
 RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
 RA Tagami M., Waki K., Watabiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
 RA Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563(2005).
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX PubMed=16141073; DOI=10.1126/science.1112009;
 RG RIKEN Genome Exploration Research Group, and Genome Science Group
 RT (Genome Network Core Team) and the FANTOM Consortium;
 RL "Antisense transcription in the Mammalian Transcriptome.";
 RL Science 309:1564-1566(2005).
 [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=22354683; PubMed=1246851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nakado I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schoenbach C., Gojohori T.,
 RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Betsel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chotcha C., Corbani L.B., Cousins S.,
 RA Dalia E., Dragani T.A., Fletcher C.F., Forrest A., Fraser K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglocz D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pereira G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Savelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Walstedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyszynski-Boris A., Yaginaka M., Yang L., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirocane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Yasuniishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Kuehlmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl L., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Watanabe Y.,
 RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Bazh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita K., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyone P., Marchionni L., Maehima J., Mazzarelli U., Mombauts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Welz C., Whitaker C., Wilming L.,
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohzuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 [7]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 [8]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
 RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
 RA Kawai J., Kojima M., Konno H., Imotani K., Nakamura M., Niimomiya N.,
 RA Nishiyori H., Nomura K., Ohno M., Muratsu M., Sano H., Sasaki D.,
 RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watabiki A.,
 RA Muramatsu M., Hayashizaki Y.;
 RT Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
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 CC -----
 CC EMBL; AK160958; BAB36114.1; -; mRNA.
 CC MG1; MG1700014; Sorb1.
 DR GO: GO:0001725; C:stress fiber; IDA.
 DR GO: GO:0005515; F:protein binding; IDA.
 DR GO: GO:0005515; F:protein binding; IPT.
 DR GO: GO:0019901; F:protein kinase binding; IDA.
 FT NON TER 1
 FT 1
 SQ SEQUENCE 14 AA; 1616 MW; 06E51JA930E0F054 CRC64;
 Query Match 31.9%; Score 23; DB 2; Length 14;
 Best Local Similarity 83.3%; Pred. No. 9e+03;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 9 VKSLYL 14
 Db 9 VKPLYL 14
 RESULT 8
 P82858_9BASI PRELIMINARY; PRT; 8 AA.
 AC P82858;
 DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
 DT 01-MAR-2001, sequence version 1.
 DE 07-FEB-2006, entry version 11.
 OS Urethase (EC 1.7.3.3) (Urate oxidase) (Fragment).
 OS Puccinia recondita f. sp. triseti.
 OC Eukaryota; Fungi; Basidiomycota; Urediniomycetes; Urediniomycetidae;
 OC Uredinales; Pucciniaaceae; Puccinia.
 NCBI_TaxID=142679;
 [1]

```

RP PROTEIN SEQUENCE, FUNCTION, AND DEVELOPMENTAL STAGE.
RC TISSUE=SPORE;
RA Aguilar M., Montalini P., Pineda M.;
RL Submitted (NOV-2000) to Swiss-Prot.
CC -!- FUNCTION: INVOLVED IN HOST-PARASITE RELATIONSHIP BETWEEN PLANTS
CC AND FUNGI.
CC -!- CATALYTIC ACTIVITY: URATE + O(2) + H(2)O = 5-HYDROXYISOURATE +
CC H(2)O(2) (5-HYDROXYISOURATE DECOMPOSE TO FORM ALLANTOIN).
CC -!- SUBCELLULAR LOCATION: PEROXISOMAL (BY SIMILARITY).
CC -!- DEVELOPMENTAL STAGE: GERMINATION.
CC -!- SIMILARITY: BELONGS TO THE URICASE FAMILY.
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-----
DR GO: GO:0005777; C:peroxisome; IEA.
DR GO: GO:0016491; F:oxidoreductase activity; IEA.
DR GO: GO:0004846; F:urate oxidase activity; IEA.
DR GO: GO:0006144; P:purine base metabolism; IEA.
DR InterPro: IPR002042; Uricase.
DR PROSITE: PS00366; URICASE; PARTIAL.
KW Oxidoreductase; Peroxisome; Purine metabolism.
FT NON_TER
SQ SEQUENCE 8 AA; 777 MW; 98CIAD735B9D76D CRC64;

Query Match
Best Local Similarity 30.6%; Score 22; DB 2; Length 8;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PFSVA 6
DB 2 PFSLA 6

RESULT 9
P92386_HORMA PRELIMINARY; PRT; 8 AA.
AC P92386;
DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1997, sequence version 1.
DT 07-FEB-2006, entry version 23.
DE Pect protein (Fragment).
GN Name=pect;
OS Hordeum marinum subsp. gussoneanum.
OC Plantae; Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BBP clade;
OC Pooidae; Triticeae; Hordeum.
OC NCBI_TaxID=98114;
OC [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=leaves;
RX MEDLINE=927271648; PubMed=9126564; DOI=10.1006/mpv.1996.0389;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
RT sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
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DR EMBL: Z77763; CAB01368.1; -; Genomic_DNA.
DR GRAMene; P92386; -.
DR GO: GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER
FT SEQUENCE 1 1
SQ SEQUENCE 8 AA; 886 MW; 1EDAB8773AE735B3 CRC64;

Query Match
Best Local Similarity 30.6%; Score 22; DB 2; Length 8;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 KSLYLIG 15

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DB 1 KSLXLIG 6

RESULT 10
Q6EOX9_YEAST PRELIMINARY; PRT; 14 AA.
AC Q6EOX9;
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE FLO1P (Fragment).
GN Name=FLO11;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OC NCBI_TaxID=4932;
OC [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=3238-32;
RX PubMed=15932987; DOI=10.1128/AEM.71.6.2934-2939.2005;
RA Zara S., Bakalinsky A.T., Zara G., Pirino G., Demontis M.A.,
RA Budroni M.;
RT "FLO11-Based Model for Air-Liquid Interfacial Biofilm Formation by
RT Saccharomyces cerevisiae.";
RL Appl. Environ. Microbiol. 71:2934-2939(2005).
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-----
DR EMBL: AY618269; AAT69750.1; -; Genomic_DNA.
DR NON_TER
FT SEQUENCE 14 AA; 1664 MW; 551F2C65193164D7 CRC64;

Query Match
Best Local Similarity 30.6%; Score 22; DB 2; Length 14;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 PFSVAKSVKSL 12
DB 4 PFLAYLVLSL 14

RESULT 11
ASPL_LACSN STANDARD; PRT; 15 AA.
AC P82648;
DT 04-MAY-2001, integrated into UniProtKB/Swiss-Prot.
DT 01-MAR-2001, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE Acid shock protein 1 (Fragment).
DE Acid shock protein 1 (Fragment).
OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OC NCBI_TaxID=1625;
OC [1]
RP PROTEIN SEQUENCE.
RC STRAIN=CB1;
RX MEDLINE=21322712; PubMed=11429463;
RA De Angelis M., Bini L., Pallini V., Coccconcelli P.S., Gobetti M.;
RT "The acid-stress response in Lactobacillus sanfranciscensis CB1.";
RL Microbiology 147:1863-1873(2001).
CC -!- INDUCTION: Overexpressed in acid environments.
-----
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-----
KW Direct protein sequencing.
FT CHAIN 1 >15
FT NON_TER
FT SEQUENCE 15 AA; 1509 MW; 575853B4DFB030A8 CRC64;

Acid shock protein 1.
/FTID=PRO_0000064703.

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Query Match 30.6%; Score 22; DB 1; Length 15;
 Best Local Similarity 66.7%; Pred. No. 1.5e+04;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 10 KSLYLIG 15
 DB 4 KGLFLG 9

RESULT 12

P93331_STRTR PRELIMINARY; PRT; 15 AA.
 AC P93331;
 DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
 DT 01-JUN-2002, sequence version 1.
 DT 07-FEB-2006, entry version 7.
 DE Penicillin-binding protein (PBP) (Fragment).
 OS Streptococcus thermophilus.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 NCBI_TaxID=1308;
 RN [1]
 RP PROTEIN SEQUENCE.
 RC STRAIN=ITG8780;
 RA Guimont C., Chopard M.A., Galliard J.L., Chamba J.F.;
 RT "Comparative study of the protein composition of three strains of
 RT Streptococcus thermophilus grown either in M17 medium or in milk."
 RL lait 0:0-0(2002).

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 CC
 DR GO: GO:0005618; C:cell wall; IEA.
 DR GO: GO:0009252; P:peptidoglycan biosynthesis; IEA.
 KM Cell wall; peptidoglycan synthesis.
 FT NON TER 1
 FT NON TER 15
 SQ SEQUENCE 15 AA; 1653 MW; 19E60997E2C4D945 CRC64;

Query Match 30.6%; Score 22; DB 2; Length 15;
 Best Local Similarity 57.1%; Pred. No. 1.5e+04;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 9 VKSLYLIG 15
 DB 1 VNSTYIG 7

RESULT 13

P92211_AGRCR PRELIMINARY; PRT; 8 AA.
 AC P92211;
 DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
 DT 01-MAY-1997, sequence version 1.
 DT 07-FEB-2006, entry version 23.
 DE Peid protein (Fragment).
 GN Name=peid;
 OS Agropyron cristatum (Created wheatgrass).
 OG Plantid; Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
 OC Poideae; Triticeae; Agropyron.
 NCBI_TaxID=4593;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Leaves;
 RA MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpcv.1996.0389;
 RA Petersen G., Seberg O.;
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
 RT sequence data."
 RL Mol. Phylogenet. Evol. 7:217-230(1997).
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 CC
 DR EMBL: Z77771; CAB01392.1; -, Genomic_DNA.
 DR GO: GO:0009507; C:chloroplast; IEA.
 KM Chloroplast.
 FT NON TER 1
 FT NON TER 1

SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 29.2%; Score 21; DB 2; Length 8;
 Best Local Similarity 83.3%; Pred. No. 2.8e+06;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 10 KSLYLIG 15
 DB 1 KSLTLG 6

RESULT 14

P92215_9POAL PRELIMINARY; PRT; 8 AA.
 ID P92215_9POAL
 AC P92215;
 DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
 DT 01-MAY-1997, sequence version 1.
 DT 07-FEB-2006, entry version 23.
 DE Peid protein (Fragment).
 GN Name=peid;
 OS Amblyopyrum muticum.
 OG Plantid; Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
 OC Poideae; Triticeae; Amblyopyrum.
 NCBI_TaxID=4595;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Leaves;
 RX MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpcv.1996.0389;
 RA Petersen G., Seberg O.;
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
 RT sequence data."
 RL Mol. Phylogenet. Evol. 7:217-230(1997).

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 CC
 DR EMBL: Z77756; CAB01347.1; -, Genomic_DNA.
 DR GO: GO:0009507; C:chloroplast; IEA.
 KM Chloroplast.
 FT NON TER 1
 FT NON TER 1

SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 29.2%; Score 21; DB 2; Length 8;
 Best Local Similarity 83.3%; Pred. No. 2.8e+06;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 10 KSLYLIG 15
 DB 1 KSLTLG 6

RESULT 15

P92222_BROIN PRELIMINARY; PRT; 8 AA.
 ID P92222_BROIN
 AC P92222;
 DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
 DT 01-MAY-1997, sequence version 1.
 DT 07-FEB-2006, entry version 23.
 DE Peid protein (Fragment).
 GN Name=peid;
 OS Bromus inermis (Smooth brome grass).
 OG Plantid; Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
 OC Poideae; Bromaeae; Bromus.

OK NCBI_TaxID=15371;
 (1)
 RN NUCLEOTIDE SEQUENCE.
 RC TISSUE=leaves;
 RX MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mprev.1996.0389;
 RA Petersen G., Seberg O.,
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
 sequence data.";
 RL Mol. Phylogenet. Evol. 7:217-230(1997).
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 CC -----
 CC EMBL: Z77759; CAB01356.1; -; Genomic_DNA.
 DR GO: GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 29.2%; Score 21; DB 2; Length 8;
 Best Local Similarity 83.3%; Pred. No. 2.8e+06;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 KSLYLG 15
 |||||
 Db 1 KSLTLG 6

RESULT 16
 P92227_CRIDE PRELIMINARY; PRT; 8 AA.
 AC P92227;
 DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
 DT 01-MAY-1997, sequence version 1.
 DT 07-FEB-2006, entry version 23.
 DE Petd protein (Fragment).
 GN Name=petd;
 OS Crithopsis delileana.
 OG Plastid; Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP clade;
 OC Pooidae; Triticeae; Crithopsis.
 NCBI_TaxID=37674;
 OK NCBI_TaxID=37674;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=leaves;
 RX MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mprev.1996.0389;
 RA Petersen G., Seberg O.,
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
 sequence data.";
 RL Mol. Phylogenet. Evol. 7:217-230(1997).
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 CC -----
 CC EMBL: Z77751; CAB01332.1; -; Genomic_DNA.
 DR GO: GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 29.2%; Score 21; DB 2; Length 8;
 Best Local Similarity 83.3%; Pred. No. 2.8e+06;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 KSLYLG 15
 |||||
 Db 1 KSLTLG 6

RESULT 17
 P92373_9POAL PRELIMINARY; PRT; 8 AA.
 ID P92373_9POAL

AC P92373;
 DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
 DT 01-MAY-1997, sequence version 1.
 DT 07-FEB-2006, entry version 23.
 DE Petd protein (Fragment).
 GN Name=petd;
 OS Haynaldia villosa.
 OG Plastid; Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP clade;
 OC Pooidae; Triticeae; Haynaldia.
 NCBI_TaxID=40247;
 OK NCBI_TaxID=40247;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=leaves;
 RX MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mprev.1996.0389;
 RA Petersen G., Seberg O.,
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
 sequence data.";
 RL Mol. Phylogenet. Evol. 7:217-230(1997).
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 CC -----
 CC EMBL: Z77741; CAB01302.1; -; Genomic_DNA.
 DR GO: GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 29.2%; Score 21; DB 2; Length 8;
 Best Local Similarity 83.3%; Pred. No. 2.8e+06;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 KSLYLG 15
 |||||
 Db 1 KSLTLG 6

RESULT 18
 P92382_9POAL PRELIMINARY; PRT; 8 AA.
 AC P92382;
 DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
 DT 01-MAY-1997, sequence version 1.
 DT 07-FEB-2006, entry version 23.
 DE Petd protein (Fragment).
 GN Name=petd;
 OS Hordeum brachyantherum.
 OG Plastid; Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP clade;
 OC Pooidae; Triticeae; Hordeum.
 NCBI_TaxID=52712;
 OK NCBI_TaxID=52712;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=leaves;
 RX MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mprev.1996.0389;
 RA Petersen G., Seberg O.,
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
 sequence data.";
 RL Mol. Phylogenet. Evol. 7:217-230(1997).
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 CC -----
 CC EMBL: Z77761; CAB01362.1; -; Genomic_DNA.
 DR Gramene; P92382; -;
 DR GO: GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 29.2%; Score 21; DB 2; Length 8;
 Best Local Similarity 83.3%; Pred. No. 2.8e+06;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 KSLYLG 15
 |||||
 1 KSLTLG 6

RESULT 19

P92384_9POAL PRELIMINARY; PRT; 8 AA.
 AC P92384;
 DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
 DT 01-MAY-1997, sequence version 1.
 DT 07-FEB-2006, entry version 23.
 DE PeD protein (Fragment).
 GN Name=peD;
 OS Hordeum murinum subsp. glaucum.
 OG Plastid; Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
 OC Poideae; Triticeae; Hordeum.
 OX NCBI_TaxID=98113;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=leaves;
 RX MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpcv.1996.0389;
 RA Petersen G., Seberg O.;
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
 sequence data.";
 RL Mol. Phylogenet. Evol. 7:217-230(1997).
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 CC -----
 CC EMBL; Z77762; CAB01365.1; -; Genomic_DNA.
 DR Gramene; P92384;
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER
 FT SEQUENCE 1 1
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 29.2%; Score 21; DB 2; Length 8;
 Best Local Similarity 83.3%; Pred. No. 2.8e+06;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 KSLYLG 15
 |||||
 1 KSLTLG 6

RESULT 20

P92388_9POAL PRELIMINARY; PRT; 8 AA.
 AC P92388;
 DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
 DT 01-MAY-1997, sequence version 1.
 DT 07-FEB-2006, entry version 23.
 DE PeD protein (Fragment).
 GN Name=peD;
 OS Henaradia persica.
 OG Plastid; Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
 OC Poideae; Triticeae; Henaradia.
 OX NCBI_TaxID=37678;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=leaves;
 RX MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpcv.1996.0389;
 RA Petersen G., Seberg O.;
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
 sequence data.";
 RL Mol. Phylogenet. Evol. 7:217-230(1997).
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 CC -----
 CC EMBL; Z77750; CAB01329.1; -; Genomic_DNA.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER
 FT SEQUENCE 1 1
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

RT sequence data.";
 RL Mol. Phylogenet. Evol. 7:217-230(1997).
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 CC -----
 CC EMBL; Z77748; CAB01323.1; -; Genomic_DNA.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER
 FT SEQUENCE 1 1
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 29.2%; Score 21; DB 2; Length 8;
 Best Local Similarity 83.3%; Pred. No. 2.8e+06;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 KSLYLG 15
 |||||
 1 KSLTLG 6

RESULT 21

P92391_HETPI PRELIMINARY; PRT; 8 AA.
 AC P92391;
 DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
 DT 01-MAY-1997, sequence version 1.
 DT 07-FEB-2006, entry version 23.
 DE PeD protein (Fragment).
 GN Name=peD;
 OS Heteranthellium piliferum.
 OG Plastid; Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
 OC Poideae; Triticeae; Heteranthellium.
 OX NCBI_TaxID=37679;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=leaves;
 RX MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpcv.1996.0389;
 RA Petersen G., Seberg O.;
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
 sequence data.";
 RL Mol. Phylogenet. Evol. 7:217-230(1997).
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 CC -----
 CC EMBL; Z77750; CAB01329.1; -; Genomic_DNA.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER
 FT SEQUENCE 1 1
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 29.2%; Score 21; DB 2; Length 8;
 Best Local Similarity 83.3%; Pred. No. 2.8e+06;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 KSLYLG 15
 |||||
 1 KSLTLG 6

RESULT 22

P92394_HORVU PRELIMINARY; PRT; 8 AA.
 AC P92394;
 DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
 DT 01-MAY-1997, sequence version 1.
 DT 07-FEB-2006, entry version 23.
 DE PeD protein (Fragment).
 GN Name=peD;
 OS Hordeum vulgare (Barley).
 RT

```

OG Plastid; Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
OC Pooidae; Triticeae; Hordeum.
OX NCBI_TaxId=4513;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=leaves;
RX MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpcv.1996.0389;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
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-----
DR EMBL; Z77764; CAB01371.1; -; Genomic_DNA.
DR Gramene; P92394; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match
Best Local Similarity 29.2%; Score 21; DB 2; Length 8;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 KSLYLG 15
DB 1 KSLTLG 6

RESULT 23
P92404 LOPEL PRELIMINARY; PRT; 8 AA.
AC P92404;
DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1997, sequence version 1.
DT 07-FEB-2006, entry version 23.
DE Pecl protein (Fragment).
GN Name=pecl;
OS Lophopyrum elongatum (Tall wheatgrass) (Aragopyrum elongatum).
OG Plastid; Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
OC Pooidae; Triticeae; Lophopyrum.
OX NCBI_TaxId=4588;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=leaves;
RX MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpcv.1996.0389;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
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-----
DR EMBL; Z77743; CAB01308.1; -; Genomic_DNA.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match
Best Local Similarity 29.2%; Score 21; DB 2; Length 8;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 KSLYLG 15
DB 1 KSLTLG 6

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RESULT 24
P92422 PSAPR PRELIMINARY; PRT; 8 AA.
AC P92422; P92420;
DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1997, sequence version 1.
DT 07-FEB-2006, entry version 21.
DE Pecl protein (Fragment).
GN Name=pecl;
OS Psathyrostachys fragilis.
OG Plastid; Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
OC Pooidae; Triticeae; Psathyrostachys.
OX NCBI_TaxId=37729;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=leaves;
RX MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpcv.1996.0389;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
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-----
DR EMBL; Z77753; CAB01338.1; -; Genomic_DNA.
DR EMBL; Z77752; CAB01335.1; -; Genomic_DNA.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match
Best Local Similarity 29.2%; Score 21; DB 2; Length 8;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 KSLYLG 15
DB 1 KSLTLG 6

RESULT 25
P92426 PSEPI PRELIMINARY; PRT; 8 AA.
AC P92426;
DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1997, sequence version 1.
DT 07-FEB-2006, entry version 23.
DE Pecl protein (Fragment).
GN Name=pecl;
OS Pseudoroegneria spicata (Bluebunch wheatgrass) (Aragopyron spicatum).
OG Plastid; Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
OC Pooidae; Triticeae; Pseudoroegneria.
OX NCBI_TaxId=4604;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=leaves;
RX MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpcv.1996.0389;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
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-----
DR EMBL; Z77744; CAB01311.1; -; Genomic_DNA.

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DR GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON TER
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 29.2%; Score 21; DB 2; Length 8;
 Best Local Similarity 83.3%; Pred. No. 2.8e+06;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 KSLYLG 15
 |||
 1 KSLTLTG 6

RESULT 26
 P92428_9POL PRELIMINARY; PRT; 8 AA.

AC P92428;
 DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
 DT 01-MAY-1997, sequence version 1.
 DT 07-FEB-2006, entry version 23.
 DE Pect protein (Fragment).

GN Name=pect;
 OS Peridictyon sanctum.
 OG Plastid; Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
 OC Poideae; Triticeae; Peridictyon.
 NCBI_TaxID=37683;

OK NCB1_TaxID=37683;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.

RC TISSUE=leaves;
 RX MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpcv.1996.0389;

RA Petersen G., Seberg O.;
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
 sequence data."

RL Mol. Phylogenet. Evol. 7:217-230(1997).

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CC EMBL; Z77749; CAB01326.1; -; Genomic_DNA.

DR GO:0009507; C:chloroplast; IEA.

KW Chloroplast.
 FT NON TER
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 29.2%; Score 21; DB 2; Length 8;
 Best Local Similarity 83.3%; Pred. No. 2.8e+06;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 KSLYLG 15
 |||
 1 KSLTLTG 6

RESULT 27
 P92431_AEGTA PRELIMINARY; PRT; 8 AA.

AC P92431;
 DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
 DT 01-MAY-1997, sequence version 1.
 DT 07-FEB-2006, entry version 24.
 DE Pect protein (Fragment).

GN Name=pect;
 OS Aegilops tauschii (Tausch's goatgrass) (Aegilops squarrosa).

OG Plastid; Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
 OC Poideae; Triticeae; Aegilops.

OK NCB1_TaxID=37682;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.

AC P92443;
 DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.

RC TISSUE=leaves;
 RX MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpcv.1996.0389;
 RA Petersen G., Seberg O.;
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
 sequence data."

RL Mol. Phylogenet. Evol. 7:217-230(1997).

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CC EMBL; Z77758; CAB01353.1; -; Genomic_DNA.

DR Gramene; P92431;
 DR GO:0009507; C:chloroplast; IEA.

KW Chloroplast.
 FT NON TER
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 29.2%; Score 21; DB 2; Length 8;
 Best Local Similarity 83.3%; Pred. No. 2.8e+06;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 KSLYLG 15
 |||
 1 KSLTLTG 6

RESULT 28

P92441_THIB PRELIMINARY; PRT; 8 AA.

AC P92441;
 DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.

DT 01-MAY-1997, sequence version 1.
 DT 07-FEB-2006, entry version 23.

DE Pect protein (Fragment).

GN Name=pect;
 OS Thinopyrum bessarabicum.

OG Plastid; Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
 OC Poideae; Triticeae; Thinopyrum.

OK NCB1_TaxID=4601;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.

RC TISSUE=leaves;
 RX MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpcv.1996.0389;

RA Petersen G., Seberg O.;
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
 sequence data."

RL Mol. Phylogenet. Evol. 7:217-230(1997).

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CC EMBL; Z77769; CAB01386.1; -; Genomic_DNA.

DR GO:0009507; C:chloroplast; IEA.

KW Chloroplast.
 FT NON TER
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 29.2%; Score 21; DB 2; Length 8;
 Best Local Similarity 83.3%; Pred. No. 2.8e+06;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 KSLYLG 15
 |||
 1 KSLTLTG 6

RESULT 29

P92443_TAECM PRELIMINARY; PRT; 8 AA.

AC P92443;
 DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.

DT 01-MAY-1997, sequence version 1.
DT 07-FEB-2006, entry version 23.
DE Petd protein (Fragment).
GN Name=petd;
OS Taeniatherum caput-medusae (Medusaehead).
OC Plastid; Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP clade;
OC Pooidae; Triticeae; Taeniatherum.
OX NCBI_TaxId=37687;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=leaves;
RX MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpev.1996.0389;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data."
RL Mol. Phylogenet. Evol. 7:217-230(1997).
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CC -----
DR EMBL: Z77760; CAB01359.1; -: Genomic_DNA.
DR GO: GO:0009507; C:chloroplast; IEA.
KM Chloroplast.
FT NON_TER 1
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 29.2%; Score 21; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 2.8e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 10 KSLYLG 15
||| ||
Db 1 KSLTIG 6

RESULT 30
P93955_FESFE PRELIMINARY; PRT; 8 AA.
ID P93955;
AC P93955;
DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1997, sequence version 1.
DT 07-FEB-2006, entry version 23.
DE Petd protein (Fragment).
GN Name=petd;
OS Festucopsis festuoides.
OC Plastid; Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP clade;
OC Pooidae; Triticeae; Festucopsis.
OX NCBI_TaxId=72455;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=leaves;
RX MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpev.1996.0389;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data."
RL Mol. Phylogenet. Evol. 7:217-230(1997).
CC -----
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CC -----
DR EMBL: Z77770; CAB01389.1; -: Genomic_DNA.
DR GO: GO:0009507; C:chloroplast; IEA.
KM Chloroplast.
FT NON_TER 1
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 29.2%; Score 21; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 2.8e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 10 KSLYLG 15
||| ||
Db 1 KSLTIG 6

RESULT 31
P93957_FESFE PRELIMINARY; PRT; 8 AA.
ID P93957;
AC P93957;
DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1997, sequence version 1.
DT 07-FEB-2006, entry version 23.
DE Petd protein (Fragment).
GN Name=petd;
OS Festucopsis sergentini.
OC Plastid; Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP clade;
OC Pooidae; Triticeae; Festucopsis.
OX NCBI_TaxId=72456;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=leaves;
RX MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpev.1996.0389;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data."
RL Mol. Phylogenet. Evol. 7:217-230(1997).
CC -----
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CC -----
DR EMBL: Z79501; CAB01777.1; -: Genomic_DNA.
DR GO: GO:0009507; C:chloroplast; IEA.
KM Chloroplast.
FT NON_TER 1
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 29.2%; Score 21; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 2.8e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 10 KSLYLG 15
||| ||
Db 1 KSLTIG 6

RESULT 32
P93959_9POAL PRELIMINARY; PRT; 8 AA.
ID P93959;
AC P93959;
DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1997, sequence version 1.
DT 07-FEB-2006, entry version 23.
DE Petd protein (Fragment).
GN Name=petd;
OS Hordeum erectifolium.
OC Plastid; Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP clade;
OC Pooidae; Triticeae; Hordeum.
OX NCBI_TaxId=58926;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=leaves;
RX MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpev.1996.0389;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data."
RL Mol. Phylogenet. Evol. 7:217-230(1997).
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CC EMBL: Z79500; CAB01776.1; -: Genomic_DNA.

DR Gramene; P93959; -

DR GO; GO:0009507; C:chloroplast; IEA.

KW Chloroplast.

FT NON TER 1

SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 29.2%; Score 21; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 2.8e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 KSLYLG 15

Db 1 KSLTLG 6

RESULT 33

P93961 PSARU PRELIMINARY; PRT; 8 AA.

AC P93961; 01-MAY-1997, integrated into UniProtKB/TrEMBL.

DT 01-MAY-1997, sequence version 1.

DE 07-FEB-2006, entry version 23.

DE Peptid protein (Fragment).

GN Name=peptid;

OS Psathyrostachys rupestris.

OC Plantae; Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;

OC Poideae; Triticeae; Psathyrostachys.

OX NCBI_TaxId=58938;

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Leaves;

RX MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpcv.1996.0389;

RA Petersen G., Seberg O.;

RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA

sequence data.";

RL Mol. Phylogenet. Evol. 7:217-230(1997).

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CC EMBL: Z77755; CAB01344.1; -: Genomic_DNA.

DR GO; GO:0009507; C:chloroplast; IEA.

KW Chloroplast.

FT NON TER 1

SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 29.2%; Score 21; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 2.8e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 KSLYLG 15

Db 1 KSLTLG 6

RESULT 34

P93963 PSAST PRELIMINARY; PRT; 8 AA.

AC P93963; 01-MAY-1997, integrated into UniProtKB/TrEMBL.

DT 01-MAY-1997, sequence version 1.

DE 07-FEB-2006, entry version 23.

DE Peptid protein (Fragment).

GN Name=peptid;

OS Psathyrostachys scoloniformis.

OC Plantae; Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;

OC Poideae; Triticeae; Psathyrostachys.

OX NCBI_TaxId=58973;

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Leaves;

RX MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpcv.1996.0389;

RA Petersen G., Seberg O.;

RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA

sequence data.";

RL Mol. Phylogenet. Evol. 7:217-230(1997).

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CC EMBL: Z77754; CAB01341.1; -: Genomic_DNA.

DR GO; GO:0009507; C:chloroplast; IEA.

KW Chloroplast.

FT NON TER 1

SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 29.2%; Score 21; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 2.8e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 KSLYLG 15

Db 1 KSLTLG 6

RESULT 35

P93965 SECST PRELIMINARY; PRT; 8 AA.

AC P93965; 01-MAY-1997, integrated into UniProtKB/TrEMBL.

DT 01-MAY-1997, sequence version 1.

DE 07-FEB-2006, entry version 23.

DE Peptid protein (Fragment).

GN Name=peptid;

OS Secale strictum.

OC Plantae; Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;

OC Poideae; Triticeae; Secale.

OX NCBI_TaxId=58866;

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Leaves;

RX MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpcv.1996.0389;

RA Petersen G., Seberg O.;

RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA

sequence data.";

RL Mol. Phylogenet. Evol. 7:217-230(1997).

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CC EMBL: Z77755; CAB01373.1; -: Genomic_DNA.

DR GO; GO:0009507; C:chloroplast; IEA.

KW Chloroplast.

FT NON TER 1

SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 29.2%; Score 21; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 2.8e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 KSLYLG 15

Db 1 KSLTLG 6

RESULT 36

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P93966_AEGSP      PRELIMINARY;   PRT;      8 AA.
ID   P93966_AEGSP
AC   P93966;
DT   01-MAY-1997, integrated into UniProtKB/TrEMBL.
DT   01-MAY-1997, sequence version 1.
DE   Petd protein (Fragment).
GN   Name=petd;
OS   Aegilops speltoides (Goatgrass).
OC   Plantae; Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep clade;
OC   Pooideae; Triticeae; Aegilops.
OX   NCBI_TaxID=4573;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=leaves.
RX   MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpev.1996.0389;
RA   Petersen G., Seberg O.;
RT   "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
RT   sequence data.";
RL   Mol. Phylogenet. Evol. 7:217-230 (1997).
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CC   -----
DR   EMBL; Z77766; CAB01377.1; -; Genomic_DNA.
DR   Gramene; P93966; -.
DR   GO; GO:0009507; C:chloroplast; IEA.
KW   Chloroplast.
FT   NON_TER
SQ   SEQUENCE      1      1
                        8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match      29.2%; Score 21; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 2.8e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      10 KSLYLG 15
Db      1 KSLTLG 6

RESULT 37
P93970_9POAL      PRELIMINARY;   PRT;      8 AA.
ID   P93970_9POAL
AC   P93970;
DT   01-MAY-1997, integrated into UniProtKB/TrEMBL.
DT   01-MAY-1997, sequence version 1.
DE   Petd protein (Fragment).
GN   Name=petd;
OS   Eremopyrum triticeum.
OC   Plantae; Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep clade;
OC   Pooideae; Triticeae; Eremopyrum.
OX   NCBI_TaxID=58937;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=leaves.
RX   MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpev.1996.0389;
RA   Petersen G., Seberg O.;
RT   "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
RT   sequence data.";
RL   Mol. Phylogenet. Evol. 7:217-230 (1997).
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CC   -----
DR   EMBL; Z77746; CAB01315.1; -; Genomic_DNA.
DR   GO; GO:0009507; C:chloroplast; IEA.
KW   Chloroplast.
FT   NON_TER
SQ   SEQUENCE      1      1
                        8 AA; 878 MW; 1EC7287731A735B3 CRC64;

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SQ   SEQUENCE      8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match      29.2%; Score 21; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 2.8e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      10 KSLYLG 15
Db      1 KSLTLG 6

RESULT 38
P93973_EREDI      PRELIMINARY;   PRT;      8 AA.
ID   P93973_EREDI
AC   P93973;
DT   01-MAY-1997, integrated into UniProtKB/TrEMBL.
DT   01-MAY-1997, sequence version 1.
DE   Petd protein (Fragment).
GN   Name=petd;
OS   Eremopyrum distans.
OC   Plantae; Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep clade;
OC   Pooideae; Triticeae; Eremopyrum.
OX   NCBI_TaxID=58936;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=leaves.
RX   MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpev.1996.0389;
RA   Petersen G., Seberg O.;
RT   "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
RT   sequence data.";
RL   Mol. Phylogenet. Evol. 7:217-230 (1997).
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CC   -----
DR   EMBL; Z77745; CAB01314.1; -; Genomic_DNA.
DR   GO; GO:0009507; C:chloroplast; IEA.
KW   Chloroplast.
FT   NON_TER
SQ   SEQUENCE      1      1
                        8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match      29.2%; Score 21; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 2.8e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      10 KSLYLG 15
Db      1 KSLTLG 6

RESULT 39
P93981_9POAL      PRELIMINARY;   PRT;      8 AA.
ID   P93981_9POAL
AC   P93981;
DT   01-MAY-1997, integrated into UniProtKB/TrEMBL.
DT   01-MAY-1997, sequence version 1.
DE   Petd protein (Fragment).
GN   Name=petd;
OS   Crotodidum monoccocum.
OC   Plantae; Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep clade;
OC   Pooideae; Triticeae; Crotodidum.
OX   NCBI_TaxID=72428;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=leaves.
RX   MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpev.1996.0389;
RA   Petersen G., Seberg O.;

```

```

RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
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DR EMBL; Z77757; CAB01350.1; -; Genomic_DNA.
DR GO; GO:0009507; C:chloroplast; IEA.
KM Chloroplast.
FT NON_TER 1
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 29.2%; Score 21; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 2.8e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 KSLYLIG 15
Db 1 KSLTLG 6

RESULT 40
P33985_AEGCM PRELIMINARY; PRT; 8 AA.
ID P33985_AEGCM
AC P33985;
DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1997, sequence version 1.
DE 07-FEB-2006, entry version 23.
DE PeetD protein (Fragment).
GN Name=peetD;
OS Aegilops comosa (Goatgrass).
OC Plastid; Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BFP clade;
OC Poideae; Triticeae; Aegilops.
OX NCBI_TaxID=4485;
[1]
RN NUCLEOTIDE SEQUENCE.
RX TISSUE=Leaves;
MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpcv.1996.0389;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
CC -----
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DR EMBL; Z77742; CAB01305.1; -; Genomic_DNA.
DR Gramene; P33985;
DR GO; GO:0009507; C:chloroplast; IEA.
KM Chloroplast.
FT NON_TER 1
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 29.2%; Score 21; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 2.8e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 KSLYLIG 15
Db 1 KSLTLG 6

RESULT 41
P33992_AUSVE PRELIMINARY; PRT; 8 AA.
ID P33992_AUSVE
AC P33992;
DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1997, sequence version 1.
DE 07-FEB-2006, entry version 23.
DE PeetD protein (Fragment).

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GN Name=peetD;
OS Australopyrum velutinum.
OC Plastid; Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BFP clade;
OC Poideae; Triticeae; Australopyrum.
OX NCBI_TaxID=58935;
[1]
RN NUCLEOTIDE SEQUENCE.
RX TISSUE=Leaves;
MEDLINE=97271648; PubMed=9126564; DOI=10.1006/mpcv.1996.0389;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
CC -----
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DR EMBL; Z77768; CAB01383.1; -; Genomic_DNA.
DR GO; GO:0009507; C:chloroplast; IEA.
KM Chloroplast.
FT NON_TER 1
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 29.2%; Score 21; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 2.8e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 KSLYLIG 15
Db 1 KSLTLG 6

RESULT 42
Q5EFY1_9BRYO PRELIMINARY; PRT; 9 AA.
ID Q5EFY1_9BRYO
AC Q5EFY1;
DT 15-MAR-2005, integrated into UniProtKB/TrEMBL.
DT 15-MAR-2005, sequence version 1.
DE 07-FEB-2006, entry version 4.
DE Cytochrome b/f complex subunit IV (Fragment).
GN Name=peetD;
OS Polytichum pallidisetum.
OC Plastid; Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Polytichopsida; Polytichales; Polytichaceae; Polytichum.
OX NCBI_TaxID=146548;
[1]
RN NUCLEOTIDE SEQUENCE.
RA Goffinet B., Wickett N.J., Shaw J.A., Cox C.J.;
RT "Phylogenetic significance of the rpoA loss in the chloroplast genome
of mosses.";
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
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DR EMBL; AY886747; AA81785.1; -; Genomic_DNA.
DR GO; GO:0009507; C:chloroplast; IEA.
KM Chloroplast.
FT NON_TER 1
SQ SEQUENCE 9 AA; 1015 MW; 45AF287731A735B3 CRC64;

Query Match 29.2%; Score 21; DB 2; Length 9;
Best Local Similarity 83.3%; Pred. No. 2.8e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 KSLYLIG 15
Db 2 KSLTLG 7

```

RESULT 43
 OSEFY7_9BRYO PRELIMINARY; PRT; 9 AA.
 AC OSEFY7;
 DT 15-MAR-2005, integrated into UniProtKB/TrEMBL.
 DT 07-FEB-2006, entry version 1.
 DE Cytochrome b/f complex subunit IV (Fragment).
 GN Name=petd;
 OS Oedipodium griffithianum.
 OC Plastid; Chloroplast.
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
 CC Polyttrichopsida; Tetraphidales; Oedipodiaceae; Oedipodium.
 CC NCBI_TaxID=127538;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Goffinet B., Wickett N.J., Shaw J.A., Cox C.J.;
 RT "Phylogenetic significance of the rpoA loss in the chloroplast genome
 of mosses.";
 RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
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 CC EMBL; AY86744; AAM81777.1; -, Genomic_DNA.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON TER
 SQ SEQUENCE 9 AA; 993 MW; 4A93287731A735B3 CRC64;

Query Match 29.2%; Score 21; DB 2; Length 9;
 Best Local Similarity 83.3%; Pred. No. 2.8e+06;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 10 KSLYLG 15
 DB 2 KSLTLG 7

RESULT 44
 OSEFZO_9BRYO PRELIMINARY; PRT; 9 AA.
 AC OSEFZO;
 DT 15-MAR-2005, integrated into UniProtKB/TrEMBL.
 DT 15-MAR-2005, sequence version 1.
 DT 07-FEB-2006, entry version 4.
 DE Cytochrome b/f complex subunit IV (Fragment).
 GN Name=petd;
 OS Buxbaumia aphylla.
 OC Plastid; Chloroplast.
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
 CC Polyttrichopsida; Tetraphidales; Buxbaumiaceae; Buxbaumia.
 CC NCBI_TaxID=70128;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Goffinet B., Wickett N.J., Shaw J.A., Cox C.J.;
 RT "Phylogenetic significance of the rpoA loss in the chloroplast genome
 of mosses.";
 RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
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 CC EMBL; AY86743; AAM81774.1; -, Genomic_DNA.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON TER
 SQ SEQUENCE 9 AA; 993 MW; 4A93287731A735B3 CRC64;

Query Match 29.2%; Score 21; DB 2; Length 9;
 Best Local Similarity 83.3%; Pred. No. 2.8e+06;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 10 KSLYLG 15
 DB 2 KSLTLG 7

RESULT 45
 O3YIM8_STRAB PRELIMINARY; PRT; 10 AA.
 AC O3YIM8;
 DT 27-SEP-2005, integrated into UniProtKB/TrEMBL.
 DT 07-FEB-2006, entry version 1.
 DE NADH dehydrogenase subunit 6 (Fragment).
 OS Strix aluco sylvatica.
 OG Mitochondrion.
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Strigiformes; Strigidae; Strix.
 CC NCBI_TaxID=340960;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA PubMed=16101775; DOI=10.1111/j.1365-294X.2005.02663.x;
 RT Brito P.H.;
 RT "The influence of Pleistocene glacial refugia on tawny owl genetic
 diversity and phylogeography in western Europe.";
 RL Mol. Ecol. 14:3077-3094(2005).
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 CC EMBL; DQ087079; AAZ77348.1; -, Genomic_DNA.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON TER
 SQ SEQUENCE 10 AA; 1238 MW; 1F934E3B572699DB CRC64;

Query Match 29.2%; Score 21; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 LYLIG 15
 DB 6 LYLIG 9

RESULT 46
 O31851_ARATH PRELIMINARY; PRT; 12 AA.
 AC O31851;
 DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
 DT 01-NOV-1996, sequence version 1.
 DT 07-FEB-2006, entry version 20.
 DE Glyceraldehyde-3-phosphate dehydrogenase (Fragment).
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Plastid; Chloroplast.
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 CC Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 CC NCBI_TaxID=3702;
 RN [1]

NUCLEOTIDE SEQUENCE.
 RP STRAIN=Columbia; TISSUE=Leaf;
 RC MEDLINE=94187724; PubMed=8139555;
 RA Conley T.R., Park S.-C., Kwon H.-B., Peng H.-S., Shih M.-C.;
 RT "Characterization of cis-acting elements in light regulation of the
 nuclear gene encoding the A subunit of chloroplast isozymes
 glyceraldehyde-3-phosphate dehydrogenase from Arabidopsis thaliana.";
 RL Mol. Cell. Biol. 14:2525-2533(1994).

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 CC EMBL; U14743; AAA31640.1; -, Genomic_DNA.
 DR GO; GO:0009507; C:chloroplast; IEA.

DR GO: 0005634; C:nucleus; IEA.
KW Chloroplast; Nuclear protein.
FT NON TER 12
SQ SEQUENCE 12 AA; 1263 MW; 81BA4C7D4BD5B9D1 CRC64;
Query Match 29.2%; Score 21; DB 2; Length 12;
Best Local Similarity 71.4%; Pred. No. 1.8e+04;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 VPFSVAK 7
DB 4 VTFSVVK 10
RESULT 47
0714T5_9CRYP PRELIMINARY; PRT; 14 AA.
AC 0714T5;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DE 07-FEB-2006, entry version 7.
DE tRNA proteolysis tag (Fragment).
GN Name=ssrA.
OS Rhodomonas salina.
OC Rhodomonas.
OG Plastid.
OC Eukaryota; Cryptophyta; Cryptomonadaceae; Rhodomonas.
OX NCBI_TaxID=52970;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CCMP1319;
RX PubMed=14681369; DOI=10.1093/nar/gkh102;
RA Guenau de Nova P., Williams K.P.;
RT "The tRNA website: reductive evolution of tRNA in plastids and other endosymbionts".
RL Nucleic Acids Res. 32:D104-D108(2004).
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CC
DR EMBL; AF550355; AAQ12671.1; -; Genomic_DNA.
FT NON TER 1
SQ SEQUENCE 14 AA; 1528 MW; D995F9B3698210B9 CRC64;
Query Match 29.2%; Score 21; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPFS 4
DB 5 VPFS 8
RESULT 48
085662_REOVJ PRELIMINARY; PRT; 14 AA.
AC 085662;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DE 07-FEB-2006, entry version 15.
DE Reovirus serotype 2 S2 (Fragment).
OS Reovirus type 2 (strain D5/Jones) (T2J) (Mammalian orthoreovirus 2).
OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
OX NCBI_TaxID=10885;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=83017877; PubMed=7123853;
RA Gailard R.K., Li J.K., Keene J.D., Joklik W.K.;
RT "The sequences at the termini of four genes of the three reovirus serotypes".
RL Virology 121:320-326(1982).
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CC
DR EMBL; J02311; AAA47250.1; -; Genomic_RNA.
FT NON TER 14
SQ SEQUENCE 14 AA; 1459 MW; 03FA0D6A8B9A30 CRC64;
Query Match 29.2%; Score 21; DB 2; Length 14;
Best Local Similarity 44.4%; Pred. No. 2.1e+04;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 6 AKSVKSLYL 14
DB 4 ARSITVGL 12
RESULT 49
09UCC2_HUMAN PRELIMINARY; PRT; 15 AA.
AC 09UCC2;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DE 07-FEB-2006, entry version 9.
DE 35 kDa heparin-RELEASABLE protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=94059921; PubMed=8241100;
RA Novotny W.F., Maffi T., Mehta R.L., Milner P.G.;
RT "Identification of novel heparin-releasable proteins, as well as the cytokines midline and pleiotrophin, in human postheparin plasma".
RL Atheroscler. Thromb. 13:1798-1805(1993).
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CC
SQ SEQUENCE 15 AA; 1456 MW; 0585FEF4FE8F6265 CRC64;
Query Match 29.2%; Score 21; DB 2; Length 15;
Best Local Similarity 44.4%; Pred. No. 2.3e+04;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 VPFSVAKSV 9
DB 6 VPIPLXKSL 14
RESULT 50
04X416_PLACH PRELIMINARY; PRT; 15 AA.
AC 04X416;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.
DE 07-FEB-2006, entry version 4.
DE Hypothetical protein (Fragment).
GN ORFNames=PC400385.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15637271; DOI=10.1126/science.1103717;
RA Hall N., Karas M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Beriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.M.,
RA Oualil M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R. III,
RA Kafatos F.C., Janse C.J., Barrell B.G., Turner C.M.R., Waters A.P.,
RA Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic, transcriptomic, and proteomic analyses.";

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RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL, CAJ01010035; CAH88301.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1713 MW; 9525B60156669C CRC64;

Query Match
Best Local Similarity 33.3%; Score 21; DB 2; Length 15;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 AKSVKSLY 14
DB 4 AKRISIVY 12

RESULT 51
ID Q714T8_9FLOR PRELIMINARY; PRT; 15 AA.
AC Q714T8;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE tRNA proteolysis tag (Fragment).
GN Name=srrA;
OS Mastocarpus papillatus.
OC Eukaryota; Rhodophyta; Florideophyceae; Gigartinales; Petrocelidaceae;
OC Macrocarpus.
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CC -----
DR EMBL, AF550352; AAQ12668.1; -; Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1735 MW; D98014394A33D2BC CRC64;

Query Match
Best Local Similarity 100.0%; Score 21; DB 2; Length 15;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFS 4
DB 6 VPFS 9

RESULT 52
ID Q7S5J5_NEUCR PRELIMINARY; PRT; 10 AA.
AC Q7S5J5;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Predicted protein.
GN ORFNames=NCU06092.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
CX NCBI_TaxID=5141;

```

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RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=74-OR23-1A / FGSC 987;
RX MEDLINE=22598136; PubMed=12712197; DOI=10.1038/nature01554;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Puccelli S., Rehman B.,
RA Ekins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Bell-Pedersen D., Nelson M.A.,
RA Werner-Mashburne M., Selitrennikoff C.P., Kinsey J.A., Braun E.L.,
RA Zelter A., Schulte U., Kothe G.O., Jedd G., Mewes H.-W., Staeben C.,
RA Marcotte E., Greenberg D., Roy A., Foley K., Naylor J.,
RA Stange-Thomann N., Barrett R., Gnerre S., Kamal M., Kamysov S.,
RA Mauceli E., Bielke C., Rudd S., Frishman D., Krystofova S.,
RA Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S., Cogoni C.,
RA Macino G., Carcheside D.E.A., Li W., Pratt R.J., Omani S.A.,
RA Desouza C.P.C., Glass N.L., Orbach M.J., Berglund J.A., Veilker R.,
RA Yarden O., Plamann W., Seiler S., Dunlap J.C., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freltag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.W.;
RT "The genome sequence of the filamentous fungus Neurospora crassa.";
RL Nature 422:859-868(2003).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL, AABX01000354; EAA30718.1; -; Genomic_DNA.
SQ SEQUENCE 10 AA; 1224 MW; 4C43FE232411B1A3 CRC64;

Query Match
Best Local Similarity 33.3%; Score 20; DB 2; Length 10;
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 5 VAKSVKSLY 13
DB 1 MAKTRKLP 9

RESULT 53
ID P83161_ANASL PRELIMINARY; PRT; 10 AA.
AC P83161;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Putative RNA-binding protein rtpA (Fragment).
OS Anabaena sp. (strain L31).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
CX NCBI_TaxID=29412;
RN [1]
RP PROTEIN SEQUENCE.
RA Apté S.K., Uhlemann E., Schmidt R., Alendort K.;
RL Submitted (OCT-2001) to Swiss-Prot.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -----
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CC -----
DR GO, GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR000504; RNP1_RNA_bd.
KW RNA-binding.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1130 MW; 1DD09AB7244862DB CRC64;

Query Match
Best Local Similarity 60.0%; Score 20; DB 2; Length 10;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 11 SLVIG 15
DB 1 SLVIG 5

```

```
RESULT 54
053VR5_MOUSE PRELIMINARY; PRT; 11 AA.
AC 053VR5;
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE D region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
NCBI_Taxid=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=66136012; PubMed=3937730;
RA Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
RT "The idiotypic network and the internal image: possible regulation of
RT a germ-line network by paucigene encoded Ab2 (anti-idiotypic)
RT antibodies in the GAT system.";
RL EMBO J. 4:3681-3688(1985).
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CC -----
DR EMBL; X03375; CAA27081.1; -; mRNA.
DR EMBL; X03374; CAA27075.1; -; mRNA.
FT NON_TER 1
FT NON_TER 11
SQ SEQUENCE 11 AA; 1318 MW; C1E17837587AB5B9 CRC64;

Query Match 27.8%; Score 20; DB 2; Length 11;
Best Local Similarity 75.0%; Pred. NO. 2.5e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFS 4
Db 2 IPFS 5

RESULT 55
086866_9VIRU PRELIMINARY; PRT; 11 AA.
ID 086866_9VIRU
AC 086866;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE S-RNA product protein (Fragment).
DE Name=S-RNA product;
OS Lymphocytic choriomeningitis virus.
OS Viruses; ssRNA negative-strand viruses; Arenaviridae; Arenavirus;
OC Old world arenaviruses.
NCBI_Taxid=11623;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95190990; PubMed=7533851;
RA Moskopidis D., Zinkernagel R.M.;
RT "Immunobiology of cytotoxic T-cell escape mutants of lymphocytic
RT choriomeningitis virus.";
RL J. Virol. 69:2187-2193(1995).
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CC -----
DR EMBL; S75748; AAB33668.1; -; mRNA.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1200 MW; 54235C80D9C45B57 CRC64;

Query Match 27.8%; Score 20; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. NO. 2.5e+04;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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```
QY 9 VKSLY 13
Db 1 IKALY 5

RESULT 56
086868_9VIRU PRELIMINARY; PRT; 11 AA.
ID 086868_9VIRU
AC 086868;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE S-RNA product protein (Fragment).
DE Name=S-RNA product;
OS Lymphocytic choriomeningitis virus.
OS Viruses; ssRNA negative-strand viruses; Arenaviridae; Arenavirus;
OC Old world arenaviruses.
NCBI_Taxid=11623;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95190990; PubMed=7533851;
RA Moskopidis D., Zinkernagel R.M.;
RT "Immunobiology of cytotoxic T-cell escape mutants of lymphocytic
RT choriomeningitis virus.";
RL J. Virol. 69:2187-2193(1995).
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CC -----
DR EMBL; S75751; AAB33671.1; -; mRNA.
FT NON_TER 11
FT NON_TER 11
SQ SEQUENCE 11 AA; 1200 MW; 54235C80D9C45B57 CRC64;

Query Match 27.8%; Score 20; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. NO. 2.5e+04;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 9 VKSLY 13
Db 1 IKALY 5

RESULT 57
HCYB_MEGCR STANDARD; PRT; 12 AA.
ID HCYB_MEGCR
AC Q10584;
DT 01-OCT-1996, integrated into UniProtKB/Swiss-Prot.
DT 01-OCT-1996, sequence version 1.
DT 07-FEB-2006, entry version 31.
DE Hemocyanin B chain (KLH-B) (Fragment).
DE Megachura crenulata (Giant keyhole limpet).
OS Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Veligastropoda; Fissurellidae; Fissurellidae; Megachura.
NCBI_Taxid=55429;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=96208935; PubMed=8829804; DOI=10.1016/0305-0491(95)02091-8;
RA Swerdlow R.D., Ebert R.F., Lee P., Bonaventura C., Miller K.I.;
RT "Keyhole limpet hemocyanin: structural and functional characterization
RT of two different subunits and multimers.";
RL Comp. Biochem. Physiol. 113B:537-548(1996).
CC -----
CC FUNCTION: Hemocyanins are copper-containing oxygen carriers
CC occurring freely dissolved in the hemolymph of many mollusks and
CC arthropods.
CC SUBUNIT: Dodecamers and extended multimers.
CC SUBCELLULAR LOCATION: Secreted protein; extracellular space.
CC TISSUE SPECIFICITY: Hemolymph.
CC BIOTECHNOLOGY: Potent immunogen used classically as a carrier
CC protein for haptens and more recently in human vaccines and for
CC immunotherapy of bladder cancer.
CC SIMILARITY: Belongs to the tyrosinase family. Hemocyanin
CC subfamily.
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CC -----
DR InterPro; IPR000896; Hemocyanin.
DR PROSITE; PS00209; HEMOCYANIN_1; PARTIAL.
DR PROSITE; PS00210; HEMOCYANIN_2; PARTIAL.
KW Copper; Direct protein sequencing; Hemolymph; Oxygen transport;
KW Transport.
FT CHAIN 1 >12 Hemocyanin B chain.
FT FTID=PRO_0000204305.
SQ SEQUENCE 12 AA; 1345 MW; CBFBEAA44A432412 CRC64;
Query Match
Best Local Similarity 27.8%; Score 20; DB 1; Length 12;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 5 VAKSVKSL 12
DB 5 VAKNVDSL 12
RESULT 58
Q945C3_CRYCO PRELIMINARY; PRT; 12 AA.
AC Q945C3;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE P80 protein (Fragment).
OS Cryptocodium cohnii (Dinoflagellate).
OC Eukaryota; Alveolata; Dinophyceae; Gonyaulacales; Cryptecodiniaceae;
OC Cryptocodium.
OX NCBI_TaxID=2866;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=9943338; PubMed=10505419;
RA Ausseil J., Soyer-Gobillard M.O., Geraud M.L., Bhaud Y., Baines I.,
RA Preston T., Moreau H.;
RT "Characterization of p80, a novel nuclear and cytoplasmic protein in
RT dinoflagellates.",
RT Procist 150:197-211(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21428164; PubMed=11545436;
RA Guillebaud D., Derelle E., Bhaud Y., Moreau H.;
RT "Role of nuclear WW domains and proline-rich proteins in
RT dinoflagellate transcription.",
RT Procist 152:127-138(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22287324; PubMed=12154093; DOI=10.1074/jbc.M205624200;
RA Guillebaud D., Sasorith S., Derelle E., Wurtz J.M., Lozano J.C.,
RA Bingham S., Tora L., Moreau H.;
RT "A new class of transcription initiation factors, intermediate between
RT TATA box-binding proteins (TBP) and TBP-like factors (TLFs), is
RT present in the marine unicellular organism, the dinoflagellate
RT Cryptocodium cohnii.",
RT J. Biol. Chem. 277:40881-40886(2002).
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CC -----
DR EMBL; AF415568; AAL15906.1; -, Genomic_DNA.
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1364 MW; 615BF873FE204414 CRC64;
Query Match
Best Local Similarity 27.8%; Score 20; DB 2; Length 12;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 5 VAKSVKSLYL 15

```

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DB : : : :
DB 1 MASARRILFIG 11
RESULT 59
Q6VSD4_9LABR PRELIMINARY; PRT; 12 AA.
AC Q6VSD4;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Ribosomal protein S7 (Fragment).
OS Thalassoma sanctaehelenae.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Labroidae;
OC Labridae; Thalassoma.
OX NCBI_TaxID=239036;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Bernardi G., Bucciarelli G., Costagliola D., Robertson R.,
RA Heiser J.B.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AY329665; AAQ86984.1; -, Genomic_DNA.
RX GO; GO:0003735; Functional constituent of ribosome; IEA.
KW Ribosomal protein.
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1310 MW; 02163AA3F9533DD4 CRC64;
Query Match
Best Local Similarity 27.8%; Score 20; DB 2; Length 12;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 AKSVKS 11
DB 6 AKIVKS 11
RESULT 60
UPE71_LITZW STANDARD; PRT; 13 AA.
AC P82050;
DT 30-MAY-2000, integrated into UniProtKB/Swiss-Prot.
DT 07-FEB-2006, entry version 1.
DE Uperin-7.1 [Contains: Uperin-7.1.1].
OS Litorea ewingi (Brown tree frog) (Ewing's tree frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae;
OC Pelodyadinae; Litorea.
OX NCBI_TaxID=104896;
RN [1]
RP PROTEIN SEQUENCE, AND MASS SPECTROMETRY.
RA Steinbomer S.T., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "An unusual combination of peptides from the skin glands of Ewing's
RT tree frog, Litorea ewingi. Sequence determination and antimicrobial
RT activity.",
RT Aust. J. Chem. 50:889-894(1997).
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CC -----

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KW Amidation; Amphibian defense peptide; Antibiotic; Antimicrobial;
KM Direct protein sequencing.
FT PEPTIDE 1 13 Uperin-7.1.
FT PEPTIDE 3 13 /FTid=PRO_0000010302.
FT PEPTIDE 3 13 Uperin-7.1.1.
FT MOD RES 13 13 /FTid=PRO_0000010303.
SQ SEQUENCE 13 AA; 1429 MW; DE17C7204CCAE322 CRC64;
Query Match 27.8%; Score 20; DB 1; Length 13;
Best Local Similarity 44.4%; Pred. No. 3e+04;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 3 FSVAKSVKS 11
DB 3 FDVVKHIAS 11
RESULT 61
Q14461 HUMAN PRELIMINARY; PRT; 13 AA.
AC Q14461_Q14842; Integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Glycophorin B (Fragment).
GN Name-GYPB;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=9026417; PubMed=1971625;
RA Rearden A., Phan H., Dubnicoff T., Kudo S., Fukuda M.;
RT "Identification of the crossing-over point of a hybrid gene encoding
human glycoprotein variant Sta. Similarity to the crossing-over point
RT in haploglobin-related genes."
RL J. Biol. Chem. 265:9259-9263(1990).
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CC -----
DR EMBL: M3505; AA53152.1; -, Genomic_DNA.
DR PIR: I70075; I70075.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1565 MW; 466944F750D145B7 CRC64;
Query Match 27.8%; Score 20; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 3e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 8 SVKSLV 13
DB 7 SIVSLV 12
RESULT 62
BRG3 RANNI STANDARD; PRT; 14 AA.
AC Q7L253;
DT 10-MAY-2004, integrated into UniProtKB/Swiss-Prot.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 15.
DE Bradykinin-like peptide 3.
OS Rana nigromaculata (Japanese pond frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana;
OC pelophylax.
OX NCBI_TaxID=8409;
RN NCB1_TaxID=8409;
RP PROTEIN SEQUENCE.

RC TISSUE=Skin;
RX MEDLINE=69117202; PubMed=5751736;
RA Nakajima T.;
RT "On the third active peptide on smooth muscle in the skin of Rana
RL nigromaculata hallowell".
RL Chem. Pharm. Bull. 16:2088-2089(1968).
CC -1- FUNCTION: Induces smooth muscle contraction.
CC -1- SUBCELLULAR LOCATION: Secreted protein.
CC -1- SIMILARITY: Belongs to the bradykinin family.
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CC -----
DR PIR: A61362; A61362.
KM Direct protein sequencing; Vasoactive; Vasodilator.
FT PEPTIDE 1 14 Bradykinin-like peptide 3.
SQ SEQUENCE 14 AA; 1486 MW; 3334EB3978393D7 CRC64;
Query Match 27.8%; Score 20; DB 1; Length 14;
Best Local Similarity 80.0%; Pred. No. 3.2e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 PFSVA 6
DB 7 PFRVA 11
RESULT 63
HCYA MEGCR STANDARD; PRT; 14 AA.
ID HCYA_MEGCR
AC Q10583;
DT 01-OCT-1996, integrated into UniProtKB/Swiss-Prot.
DT 01-OCT-1996, sequence version 1.
DT 07-FEB-2006, entry version 29.
DE Hemocyanin A chain (KLM-A) (Fragment).
OS Megachura crenulata (Giant keyhole limpet).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orchoastropoda;
OC Veriastropoda; Fissurellioidea; Fissurellidae; Megachura.
OX NCBI_TaxID=55429;
RN NCB1_TaxID=55429;
RP PROTEIN SEQUENCE.
RA MEDLINE=96208935; PubMed=8229804; DOI=10.1016/0305-0491(95)02091-8;
RX Smerlow R.D., Ebert R.F., Lee P., Bonaventura C., Miller K.I.;
RT "keyhole limpet hemocyanin: structural and functional characterization
RT of two different subunits and multimers".
RL Comp. Biochem. Physiol. 113B:537-548(1996).
CC -1- FUNCTION: Hemocyanins are copper-containing oxygen carriers
CC occurring freely dissolved in the hemolymph of many mollusks and
CC arthropods.
CC -1- SUBUNIT: Decamers and didecamers.
CC -1- SUBCELLULAR LOCATION: Secreted protein; extracellular space.
CC -1- TISSUE SPECIFICITY: Hemolymph.
CC -1- BIOTECHNOLOGY: Potent immunogen used classically as a carrier
CC protein for haptens and more recently in human vaccines and for
CC immunotherapy of bladder cancer.
CC -1- SIMILARITY: Belongs to the tyrosinase family. Hemocyanin
CC subfamily.
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CC -----
DR InterPro: IPR000896; Hemocyanin.
DR PROSITE: PS00209; HEMOCYANIN_1; PARTIAL.
DR PROSITE: PS00210; HEMOCYANIN_2; PARTIAL.
KM Copper; Direct protein sequencing; Hemolymph; Oxygen transport;
KM Transport.
FT CHAIN 1 >14 Hemocyanin A chain.
FT NON_TER 14 14 /FTid=PRO_0000204304.
SQ SEQUENCE 14 AA; 1610 MW; 9CE61977014A99D5 CRC64;
Query Match 27.8%; Score 20; DB 1; Length 14;

Best Local Similarity 62.5%; Pred. No. 3.2e+04;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 VAKSVKSL 12
| | | | |
DB 4 VAKSVKSL 11

RESULT 64

096050 HUMAN

ID 096050 HUMAN PRELIMINARY; PRT; 14 AA.

AC 096050

DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.

DT 01-DEC-2001, sequence version 1.

DT 07-FEB-2006, entry version 9.

DE Mitochondrial ribosomal protein L33 (Fragment).

GN Name=MRPL33;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;

OC Homo.

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=21429115; PubMed=11543634; DOI=10.1006/geno.2001.6622;

RA Kennicht N., Suzuki T., Uechi T., Magoor M., Kuniba M., Higa S.,

RA Watanabe K., Tanaka T.;

RT "The human mitochondrial ribosomal protein genes: mapping of 54 genes

to the chromosomes and implications for human disorders.";

RL Genomics 77:65-70(2001).

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CC EMBL, AB051623; BAB54951.1; -; Genomic DNA.

DR GO: GO:0003735; F:structural constituent of ribosome; IEA.

KW Ribosomal protein.

FT NON_TER 1 1

SQ SEQUENCE 14 AA; 1744 MW; 64ED243B9AED63B CRC64;

Query Match 27.8%; Score 20; DB 2; Length 14;

Best Local Similarity 41.7%; Pred. No. 3.2e+04;

Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 VPSVAKSVKSL 12
| | | | |
DB 3 VLFVEKKKIRSL 14

RESULT 65

038205 LACSS

ID 038205 LACSS PRELIMINARY; PRT; 15 AA.

AC 038205

DT 22-NOV-2005, integrated into UniProtKB/TrEMBL.

DT 22-NOV-2005, sequence version 1.

DT 07-MAR-2006, entry version 4.

DE Hypothetical small peptide.

GN OrderedlocusNames=LSA0083;

OS Lactobacillus sakei subsp. sakei (strain 23K).

OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;

OC Lactobacillus.

OX NCBI_TaxID=314315;

RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RX PubMed=16273110; DOI=10.1038/nbt1160;

RA Chailion S., Champomier-Verges M.-C., Cornet M., Cruz-Le Cog A.-M.,

RA Duzet A.-M., Martin V., Beaufils S., Darbon-Rongere E., Bossy R.,

RA Loux V., Zagorec M.;

RT "The complete genome sequence of the meat-borne lactic acid bacterium

Lactobacillus sakei 23K.";

RL Nat. Biotechnol. 23:1527-1533 (2005).

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DR EMBL, CR936503; CA154382.1; -; Genomic DNA.

DR GenomeReviews; CR936503.GR; LSA0083.

KW Complete proteome; Hypothetical protein.

SQ SEQUENCE 15 AA; 1676 MW; 95F386574D90FEB3 CRC64;

Query Match 27.8%; Score 20; DB 2; Length 15;
Best Local Similarity 60.0%; Pred. No. 3.5e+04;

Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 SVAKSVKSLY 13
| | | | |
DB 2 SVDKSVDCGY 11

RESULT 66

070788 GLAMI

ID 070788 GLAMI PRELIMINARY; PRT; 8 AA.

AC 070788

DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.

DT 05-JUL-2004, sequence version 1.

DT 07-FEB-2006, entry version 8.

DE Ribosomal protein (Fragment).

GN Name=rp16;

OS Placostoma fimbriatum.

OG Placostoma.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

OC asterids; lamiales; Lamiales; Lamiaceae; Nepetoideae; Ocineae;

OC Placostoma.

OX NCBI_TaxID=204168;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX PubMed=15019625; DOI=10.1016/j.ymprev.2003.08.002;

RA Paton A., Springate D.A., Sude S., Ojien D., Grayer R., Harley M.M.,

RA Willis F., Simmonds W.S.J., Powell M.P., Savolainen V.;

RT "Phylogeny and evolution of basilis and allies (Ocineae, Labiales)

based on three plastid DNA regions.";

RL Mol. Phylogenet. Evol. 31:277-299(2004).

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CC EMBL, AJ505368; CAD45489.1; -; Genomic DNA.

DR GO: GO:0003735; F:structural constituent of ribosome; IEA.

KW Ribosomal protein.

FT NON_TER 1 1

SQ SEQUENCE 8 AA; 789 MW; 86786772D1BBA772 CRC64;

Query Match 26.4%; Score 19; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 2.8e+06;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPSV 5
| | | | |
DB 1 VPYTV 5

RESULT 67

06UIQ3 MACMU

ID 06UIQ3 MACMU PRELIMINARY; PRT; 9 AA.

AC 06UIQ3

DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.

DT 05-JUL-2004, sequence version 1.

DT 07-FEB-2006, entry version 6.

DE Glutamine-fructose-6-phosphate transaminase 1 (Fragment).

GN Name=GFPT1;

OS Macaca mulatta (Rhesus macaque).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

OC Cercopithecoidea; Cercopithecoidea; Macaca.

OX NCBI_TaxID=9544;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22946167; PubMed=14557539; DOI=10.1073/pnas.2135499100;
 RA Caceres M., Lachner J., Zapala M.A., Redmond J.C., Kudo L.,
 RA Geschwind D.H., Lockhart D.J., Preuss T.M., Barlow C.,
 RT "Elevated gene expression levels distinguish human from non-human
 RT primate brains";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:13030-13035(2003).
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 CC -----
 DR EMBL: AY369811; AAR1242.1; -; mRNA.
 FT NON TER 1
 SQ SEQUENCE 9 AA: 960 MW; SBF4D1B2D5B33DD7 CRC64;
 QY Query Match 26.4%; Score 19; DB 2; Length 9;
 Best Local Similarity 66.7%; Pred. No. 2.8e+06;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 4 SVAKSV 9
 Db :|||||
 1 NLAKSV 6
 RESULT 68
 ID Q607P3_RALEU PRELIMINARY; PRT; 9 AA.
 AC Q607P3;
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 5.
 DE Glucosamine synthetase (Fragment).
 GN Name=glnS;
 OS Ralstonia eutropha (Alcaligenes eutrophus).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Cupriavidus.
 OX NCBI_TaxID=106590;
 RN [1]
 RN NUCLEOTIDE SEQUENCE.
 RA Aspray T.J., Burns R.G.;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL: AY553854; AAS66992.1; -; Genomic_DNA.
 FT NON TER 1
 SQ SEQUENCE 9 AA: 960 MW; SBF4D1B2D5B33DD7 CRC64;
 QY Query Match 26.4%; Score 19; DB 2; Length 9;
 Best Local Similarity 66.7%; Pred. No. 2.8e+06;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 4 SVAKSV 9
 Db :|||||
 1 NLAKSV 6
 RESULT 69
 ID Q476S1_ECOLI PRELIMINARY; PRT; 10 AA.
 AC Q476S1;
 DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
 DT 01-NOV-1996, sequence version 1.
 DT 07-FEB-2006, entry version 24.
 DE TrpA protein (Fragment).
 GN Name=trpA;
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.

OX NCBI_TaxID=562;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=K-12;
 RX MEDLINE=88118903; PubMed=3323526;
 RA Jallajakumari M.B., Guidolin A., Buhj H.J., Manning P.A.;
 RT "Surface exclusion genes trsA and trsB of the F sex factor of
 RT Escherichia coli K-12. Determination of the nucleotide sequence and
 RT promoter and terminator activities";
 RL J. Mol. Biol. 198:1-11(1987).
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 CC -----
 DR EMBL: D90177; BAA14207.1; -; Genomic_DNA.
 KM Plasmid.
 FT NON TER 1
 SQ SEQUENCE 10 AA: 1070 MW; CCI8014DD045B33D CRC64;
 QY Query Match 26.4%; Score 19; DB 2; Length 10;
 Best Local Similarity 37.5%; Pred. No. 3.5e+04;
 Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 5 VAKSVKSL 12
 Db :|||||
 2 LAKSIANI 9
 RESULT 70
 ID Q9UCP2_HUMAN PRELIMINARY; PRT; 11 AA.
 AC Q9UCP2;
 DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
 DT 01-MAY-2000, sequence version 1.
 DT 07-FEB-2006, entry version 9.
 DE CGMP-inhibited LOW K(M) cAMP phosphodiesterase PEAK 43, CGI-PDE
 DE (Fragment).
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RN PROTEIN SEQUENCE.
 RP MEDLINE=92283180; PubMed=1317779; DOI=10.1210/en.130.6.3265;
 RA Lebon T.R., Kasuya J., Paxton R.J., Belfrage P., Hockman S.,
 RA Manganiello V.C., Fujita Yamaguchi Y.;
 RT "Purification and characterization of guanosine 3',5'-monophosphate-
 RT inhibited low K(M) adenosine 3',5'-monophosphate phosphodiesterase
 RT from human placental cytosolic fractions";
 RL Endocrinology 130:3265-3274(1992).
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 CC -----
 DR GO: GO:0005829; Cytosol; TAS.
 DR GO: GO:0004115; FcAMP-specific phosphodiesterase activity; TAS.
 DR GO: GO:0007165; P signal transduction; NAS.
 FT NON TER 1
 SQ SEQUENCE 11 AA: 1220 MW; 7DF1PDP2D44735BB CRC64;
 QY Query Match 26.4%; Score 19; DB 2; Length 11;
 Best Local Similarity 27.3%; Pred. No. 3.8e+04;

Matches 3; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 4 SVAKSVKSLYL 14
|:|:|:|:
Db 1 SLNESUNALFT 11

RESULT 71
059AX1 9COLE PRELIMINARY; PRT; 11 AA.
AC 059AX1-
DT 26-APR-2005, integrated into UniProtKB/TrEMBL.
DT 26-APR-2005, sequence version 1.
DE 07-FEB-2006, entry version 5.
DE NADH dehydrogenase subunit 1 (Fragment).
GN Name=NADH1;
OS Cicindela (Rivacindela) sp. JP-36.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Adephaga; Cicindelidae;
OC Cicindela; Rivacindela.
OX NCBI_TaxId=258626;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=36_4;
RX PubMed=15647517; DOI=10.1093/molbev/msi085;
RA Pons J., Vogler A.;
RT "Complex Pattern of Coalescence and Fast Evolution of a Mitochondrial
rRNA Pseudogene in a Recent Radiation of Tiger Beetles";
RL Mol. Biol. Evol. 22:991-1000(2005).
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CC -----
DR EMBL; AJ619231; CAG18254.1; -; Genomic_DNA.
DR GO; GO:0005739; Mitochondrion; IEA.
KM Mitochondrion.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1283 MW; 220384AE27272AA8 CRC64;

Query Match 26.4%; Score 19; DB 2; Length 11;
Best Local Similarity 75.0%; Pred. No. 3.8e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 LYLG 15
|:|:|:
Db 1 MYLG 4

RESULT 72
05UIX7 9FLOR PRELIMINARY; PRT; 12 AA.
AC 05UIX7-
DT 07-DEC-2004, integrated into UniProtKB/TrEMBL.
DT 07-DEC-2004, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Cytochrome oxidase subunit 3 (Fragment).
OS Gracilaria vermiculophylla.
OC Mitochondrion.
OC Eukaryota; Rhodophyta; Florideophyceae; Gracilariaceae;
OC Gracilaria.
OX NCBI_TaxId=257814;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Ruessens J.;
RT "Life history and molecular sequences of Gracilaria vermiculophylla
(Gracilariaceae, Rhodophyta), a new introduction to European waters.";
RL Phycologia 0:0-0(2005).
CC -----
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CC -----
DR EMBL; AY725143; AAV51349.1; -; Genomic_DNA.

DR GO; GO:0005739; Mitochondrion; IEA.
KM Mitochondrion.
FT NON_TER 12
SQ SEQUENCE 12 AA; 1383 MW; 87F0F2C11CA2D6C5 CRC64;

Query Match 26.4%; Score 19; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 4.2e+04;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 VAKSVK 10
|:|:|:|:
Db 7 VAKSVQ 12

RESULT 73
06PAJ9 MOUSE PRELIMINARY; PRT; 12 AA.
AC 06PAJ9;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DE 07-FEB-2006, entry version 11.
DE D11WSu47e protein.
GN Name=D11WSu47e;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shamen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carinci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strussberg R.;
RT Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; BC060257; AAH60257.1; -; mRNA.
DR MGI; MGI:106356; D11WSu47e.
SQ SEQUENCE 12 AA; 1262 MW; DFE49D95A4D33DC2 CRC64;

Query Match 26.4%; Score 19; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 4.2e+04;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 SVAKSV 9
|:|:|:|:
Db 4 SVAKAM 9

RESULT 74
Dahl1_LITDA STANDARD; PRT; 13 AA.
AC P84273;
DT 23-NOV-2004, integrated into UniProtKB/Swiss-Prot.
DT 23-NOV-2004, sequence version 1.
DE Dahlein-1.1.
OS Litoria dahlia (Dahl's aquatic frog).
OC Eukaryota; Metazoa; Chordata; Cranata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hyllidae;
OC Pelodytidae; Litoria.
OX NCBI_TaxID=299727;
RN [1]
RP PROTEIN SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, TISSUE SPECIFICITY,
AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX PubMed=11555873; DOI=10.1002/rcm.429;
RA Wegener K.L., Brinkworth C.S., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "Bioactive dahlia peptides from the skin secretions of the Australian
aquatic frog Litoria dahlia: sequence determination by electrospray
mass spectrometry.";
RT Rapid Commun. Mass Spectrom. 15:1726-1734(2001).
CC -1- FUNCTION: Weak wide spectrum antimicrobial activity against Gram-
positive bacteria.
CC -1- SUBCELLULAR LOCATION: Secreted protein.
CC -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -1- MASS SPECTROMETRY: MW=1430; METHOD=Electrospray; RANGE=1-13;
CC NOTE=Ref.1.

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GO; GO:0005576; C:extracellular region; IDA.
DR GO; GO:0050830; P:defense response to Gram-positive bacteria; IDA.
DR InterPro; IPR013157; Antimicrobial_20.
DR Pfam; PF08256; Antimicrobial20; 1.
KW Amphibian defense peptide; Antibiotic; Antimicrobial;
KW Direct protein sequencing.
FT PEPTIDE 1 13 Dahlein-1.1.
FT /FTID=PRO_0000043772.
SQ SEQUENCE 13 AA; 1433 MW; 1048B722BECF330 CRC64;
Query Match 26.4%; Score 19; DB 1; Length 13;
Best Local Similarity 33.3%; Pred. No. 4.6e+04;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
OY 3 PSVAKSVK 11
DB 3 FDIKNIVS 11

RESULT 75
ID SAH11 POPEU STANDARD; PRT; 13 AA.
AC P84533;
DT 21-JUN-2005, integrated into UniProtKB/Swiss-Prot.
DT 21-JUN-2005, sequence version 1.
DE Adenosylhomocysteine 1 (EC 3.3.1.1) (S-adenosyl-L-homocysteine
hydrolase) (AdoHcyase) (Fragment).
OS Populus euphratica (Euphrates poplar).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eustosids I; Malpighiales; Salicaceae; Saliceae; Populus.
OX NCBI_TaxID=75702;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Leaf;
RA Ferreira S., Hjerno K., Larsen M., Wingsle G., Larsen P., Fey S.,
RA Roepstorff P., Pals M.S.;
RT "Proteome profiling of Populus euphratica Oliv. upon heat stress.";
RT Submitted (APR-2005) to Swiss-Prot.
CC -1- FUNCTION: Adenosylhomocysteine is a competitive inhibitor of S-
adenosyl-L-methionine-dependent methyl transferase reactions;
therefore adenosylhomocysteine may play a key role in the
control of methylations via regulation of the intracellular
concentration of adenosylhomocysteine (By similarity).
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = L-
homocysteine + adenosine.
CC -1- COFACTOR: Binds 1 NAD per subunit (By similarity).
CC -1- PATHWAY: Activated methyl cycle.
CC -1- SUBUNIT: Homotetramer (By similarity).
CC -1- SIMILARITY: Belongs to the adenosylhomocysteine family.

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DR InterPro; IPR000043; Ad_hcy_hydrolase.
DR PROSITE; PS00738; ADOHCYASE_1; PARTIAL.
KW Direct protein sequencing; Hydrolase; NAD; One-carbon metabolism.
FT CHAIN <1 >13 Adenosylhomocysteine 1.
FT /FTID=PRO_0000116930.
FT NON TER 1 1
FT NON TER 13 13
SQ SEQUENCE 13 AA; 1394 MW; 897A15F868D376C5 CRC64;
Query Match 26.4%; Score 19; DB 1; Length 13;
Best Local Similarity 66.7%; Pred. No. 4.6e+04;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 2 PSVAK 7
DB 8 PFKGAK 13

RL Submitted (APR-2005) to Swiss-Prot.
CC -1- FUNCTION: Adenosylhomocysteine is a competitive inhibitor of S-
adenosyl-L-methionine-dependent methyl transferase reactions;
therefore adenosylhomocysteine may play a key role in the
control of methylations via regulation of the intracellular
concentration of adenosylhomocysteine (By similarity).
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = L-
homocysteine + adenosine.
CC -1- COFACTOR: Binds 1 NAD per subunit (By similarity).
CC -1- PATHWAY: Activated methyl cycle.
CC -1- SUBUNIT: Homotetramer (By similarity).
CC -1- SIMILARITY: Belongs to the adenosylhomocysteine family.

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DR InterPro; IPR000043; Ad_hcy_hydrolase.
DR PROSITE; PS00738; ADOHCYASE_1; PARTIAL.
KW Direct protein sequencing; Hydrolase; NAD; One-carbon metabolism.
FT CHAIN <1 >13 Adenosylhomocysteine 1.
FT /FTID=PRO_0000116930.
FT NON TER 1 1
FT NON TER 13 13
SQ SEQUENCE 13 AA; 1394 MW; 897A15F868D376C5 CRC64;
Query Match 26.4%; Score 19; DB 1; Length 13;
Best Local Similarity 66.7%; Pred. No. 4.6e+04;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 2 PSVAK 7
DB 8 PFKGAK 13

RESULT 76
ID SAH2 POPEU STANDARD; PRT; 13 AA.
AC P84532;
DT 21-JUN-2005, integrated into UniProtKB/Swiss-Prot.
DT 21-JUN-2005, sequence version 1.
DE Adenosylhomocysteine 2 (EC 3.3.1.1) (S-adenosyl-L-homocysteine
hydrolase) (AdoHcyase) (Fragment).
OS Populus euphratica (Euphrates poplar).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eustosids I; Malpighiales; Salicaceae; Saliceae; Populus.
OX NCBI_TaxID=75702;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Leaf;
RA Ferreira S., Hjerno K., Larsen M., Wingsle G., Larsen P., Fey S.,
RA Roepstorff P., Pals M.S.;
RT "Proteome profiling of Populus euphratica Oliv. upon heat stress.";
RT Submitted (APR-2005) to Swiss-Prot.
CC -1- FUNCTION: Adenosylhomocysteine is a competitive inhibitor of S-
adenosyl-L-methionine-dependent methyl transferase reactions;
therefore adenosylhomocysteine may play a key role in the
control of methylations via regulation of the intracellular
concentration of adenosylhomocysteine (By similarity).
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = L-
homocysteine + adenosine.
CC -1- COFACTOR: Binds 1 NAD per subunit (By similarity).
CC -1- PATHWAY: Activated methyl cycle.
CC -1- SUBUNIT: Homotetramer (By similarity).
CC -1- SIMILARITY: Belongs to the adenosylhomocysteine family.

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DR InterPro; IPR000043; Ad_hcy_hydrolase.
DR PROSITE; PS00738; ADOHCYASE_1; PARTIAL.

DR PROSITE, PS00739; ADOHCYASE 2; PARTIAL.
KM Direct protein sequencing; Hydrolase; NAD; One-carbon metabolism.
FT CHAIN <1 >13 Adenosylhomocysteinease 2.
FT /FTId=PRO_0000116931.
FT NON_TER 1 1
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1364 MW; 897A15F878D276C5 CRC64;

Query Match
Best Local Similarity 26.4%; Score 19; DB 1; Length 13;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PPSVAK 7
Db 8 PFGAK 13

RESULT 77
ID 097122_TOXGO PRELIMINARY; PRT; 13 AA.
AC 097122;
DT 01-MAY-1999, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1999, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Ycf24 protein (Fragment).
GN Name=ycf24;
OS Toxoplasma gondii.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;
OC Toxoplasma.
OX NCBI_TaxID=5811;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=RH;
RA Aiello D.P., Lang-Umansch N.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL, AF095904; AADI7841.1; -; Genomic_DNA.
FT NON_TER 1 1
SQ SEQUENCE 13 AA; 1532 MW; CC8DB4011FCDC40D CRC64;

Query Match
Best Local Similarity 26.4%; Score 19; DB 2; Length 13;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 VAKSVKSLY 13
Db 5 VARAKLIFY 13

RESULT 78
ID 09U7D6_NEOCA PRELIMINARY; PRT; 13 AA.
AC 09U7D6;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Ycf24 protein (Fragment).
GN Name=ycf24;
OS Neospora caninum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;
OC Neospora.
OX NCBI_TaxID=29176;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NC1;
RA MEDLINE=20074141, PubMed=10608442; DOI=10.1016/S0020-7519(99)00119-8;
RA Lang-Umansch N., Aiello D.P.;
RT "Sequence evidence for an altered genetic code in the Neospora caninum
RT plasmid";
RL Int. J. Parasitol. 29:1557-1562(1999).

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CC -----
DR EMBL, AF138960; AAF14260.1; -; Genomic_DNA.
FT NON_TER 1 1
SQ SEQUENCE 13 AA; 1532 MW; CC8DB4011FCDC40D CRC64;

Query Match
Best Local Similarity 26.4%; Score 19; DB 2; Length 13;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 VAKSVKSLY 13
Db 5 VARAKLIFY 13

RESULT 79
ID 050038_MYCLE PRELIMINARY; PRT; 13 AA.
AC 050038;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE U22661.
OS Mycobacterium leprae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Smith D.R.;
RA Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Robison K.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL, U15182; AAA62970.1; -; Genomic_DNA.
SQ SEQUENCE 13 AA; 1589 MW; C7CCD7E47D025B06 CRC64;

Query Match
Best Local Similarity 26.4%; Score 19; DB 2; Length 13;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 VKSLYLG 15
Db 4 VQOEYLG 10

RESULT 80
ID 04XAS9_PLACH PRELIMINARY; PRT; 14 AA.
AC 04XAS9;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Hypothetical protein.
GN ORFNames=PC404082.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15637271; DOI=10.1126/science.1103717;
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.M.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R. III,

RA Kafatos F.C., Janse C.J., Barrell B.G., Turner C.M.R., Waters A.P.,
RA Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses."; Science 307:82-86(2005).
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
CC EMBL; CAJ01008150; CAH85994.1; -; Genomic_DNA.
DR Hypothetical protein.
KM SEQUENCE 14 AA; 1709 MW; 8C5EE17FC3A90CA1 CRC64;
SQ
Query Match 26.4%; Score 19; DB 2; Length 14;
Best Local Similarity 57.1%; Pred. No. 4.9e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 8 SVKSLYL 14
| : |||
Db 8 SLHKLYL 14

Search completed: July 12, 2006, 05:39:16
Job time : 317 secs

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OM protein - protein search, using sw model

Run on: July 12, 2006, 05:51:00 ; Search time 174 Seconds
(without alignments)
39.932 Million cell updates/sec

Title: US-10-671-019-2

Perfect score: 72
Sequence: 1 VPFSVAKSVKSLYLIG 15

Scoring table:

BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 395127

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 800 summaries

Database :

Published Applications_AA_Main:*

- 1: /EMC_Celextra_SIDS3/prodata/2/pubppaa/US07_PUBCOMB.pep:*
- 2: /EMC_Celextra_SIDS3/prodata/2/pubppaa/US08_PUBCOMB.pep:*
- 3: /EMC_Celextra_SIDS3/prodata/2/pubppaa/US09_PUBCOMB.pep:*
- 4: /EMC_Celextra_SIDS3/prodata/2/pubppaa/US10A_PUBCOMB.pep:*
- 5: /EMC_Celextra_SIDS3/prodata/2/pubppaa/US10B_PUBCOMB.pep:*
- 6: /EMC_Celextra_SIDS3/prodata/2/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	40.3	9	US-10-884-862-219	Sequence 219, App
2	28	38.9	7	US-10-820-067A-361	Sequence 361, App
3	28	38.9	8	US-10-776-521B-152	Sequence 152, App
4	28	38.9	8	US-10-820-067A-648	Sequence 648, App
5	27	37.5	15	US-10-943-793-17	Sequence 17, App
6	26	36.1	11	US-09-852-910-81	Sequence 81, App
7	26	36.1	11	US-10-411-336A-81	Sequence 81, App
8	26	36.1	12	US-09-563-222-35	Sequence 35, App
9	26	36.1	12	US-10-461-878-1	Sequence 1, App
10	26	36.1	12	US-10-783-950-35	Sequence 35, App
11	26	36.1	12	US-10-461-885-1	Sequence 1, App
12	26	36.1	12	US-10-507-662-11	Sequence 11, App
13	26	36.1	14	US-09-820-649-319	Sequence 319, App
14	26	36.1	14	US-10-160-162-319	Sequence 319, App
15	26	36.1	14	US-10-936-773-319	Sequence 319, App
16	26	36.1	15	US-09-907-969-500	Sequence 500, App
17	26	36.1	15	US-10-198-053-500	Sequence 500, App
18	26	36.1	15	US-10-431-096-289	Sequence 289, App
19	26	36.1	15	US-10-860-790-500	Sequence 500, App
20	25.5	35.4	14	US-10-676-909-53	Sequence 53, App
21	25.5	35.4	15	US-10-676-909-54	Sequence 54, App
22	25	34.7	8	US-09-920-480B-9	Sequence 9, App
23	25	34.7	8	US-10-333-430-17	Sequence 17, App
24	25	34.7	9	US-09-847-185-30	Sequence 30, App
25	25	34.7	9	US-09-862-260A-3	Sequence 3, App
26	25	34.7	9	US-09-862-260A-23	Sequence 23, App
27	25	34.7	9	US-09-923-831-31	Sequence 31, App

28	25	34.7	9	US-09-872-832-45	Sequence 45, App
29	25	34.7	9	US-09-766-889A-43	Sequence 43, App
30	25	34.7	9	US-09-812-238B-3	Sequence 3, App
31	25	34.7	9	US-09-812-238B-5	Sequence 5, App
32	25	34.7	9	US-09-812-238B-7	Sequence 7, App
33	25	34.7	9	US-09-812-238B-9	Sequence 9, App
34	25	34.7	9	US-09-812-238B-11	Sequence 11, App
35	25	34.7	9	US-09-812-238B-13	Sequence 13, App
36	25	34.7	9	US-09-812-238B-15	Sequence 15, App
37	25	34.7	9	US-09-812-238B-17	Sequence 17, App
38	25	34.7	9	US-09-812-238B-19	Sequence 19, App
39	25	34.7	9	US-09-909-460-62	Sequence 62, App
40	25	34.7	9	US-09-865-548A-42	Sequence 42, App
41	25	34.7	9	US-09-898-860-83	Sequence 83, App
42	25	34.7	9	US-09-898-860-84	Sequence 84, App
43	25	34.7	9	US-09-898-860-85	Sequence 85, App
44	25	34.7	9	US-09-898-860-86	Sequence 86, App
45	25	34.7	9	US-09-898-860-87	Sequence 87, App
46	25	34.7	9	US-09-898-860-88	Sequence 88, App
47	25	34.7	9	US-09-898-860-89	Sequence 89, App
48	25	34.7	9	US-09-898-860-90	Sequence 90, App
49	25	34.7	9	US-09-898-860-91	Sequence 91, App
50	25	34.7	9	US-09-898-860-92	Sequence 92, App
51	25	34.7	9	US-09-898-860-93	Sequence 93, App
52	25	34.7	9	US-09-898-860-94	Sequence 94, App
53	25	34.7	9	US-09-898-860-95	Sequence 95, App
54	25	34.7	9	US-09-898-860-96	Sequence 96, App
55	25	34.7	9	US-09-898-860-97	Sequence 97, App
56	25	34.7	9	US-09-898-860-98	Sequence 98, App
57	25	34.7	9	US-09-898-860-99	Sequence 99, App
58	25	34.7	9	US-09-898-860-100	Sequence 100, App
59	25	34.7	9	US-09-898-860-101	Sequence 101, App
60	25	34.7	9	US-09-898-860-102	Sequence 102, App
61	25	34.7	9	US-09-898-860-103	Sequence 103, App
62	25	34.7	9	US-09-920-480B-5	Sequence 5, App
63	25	34.7	9	US-09-920-480B-6	Sequence 6, App
64	25	34.7	9	US-09-920-480B-7	Sequence 7, App
65	25	34.7	9	US-09-920-480B-8	Sequence 8, App
66	25	34.7	9	US-10-161-097-28	Sequence 28, App
67	25	34.7	9	US-10-161-097-29	Sequence 29, App
68	25	34.7	9	US-10-161-097-30	Sequence 30, App
69	25	34.7	9	US-10-161-097-31	Sequence 31, App
70	25	34.7	9	US-10-161-097-32	Sequence 32, App
71	25	34.7	9	US-10-161-097-33	Sequence 33, App
72	25	34.7	9	US-10-161-097-34	Sequence 34, App
73	25	34.7	9	US-10-161-097-35	Sequence 35, App
74	25	34.7	9	US-10-161-097-36	Sequence 36, App
75	25	34.7	9	US-10-161-097-37	Sequence 37, App
76	25	34.7	9	US-10-161-097-38	Sequence 38, App
77	25	34.7	9	US-10-161-097-39	Sequence 39, App
78	25	34.7	9	US-10-161-097-40	Sequence 40, App
79	25	34.7	9	US-10-161-097-41	Sequence 41, App
80	25	34.7	9	US-10-161-097-42	Sequence 42, App
81	25	34.7	9	US-10-161-097-43	Sequence 43, App
82	25	34.7	9	US-10-161-097-44	Sequence 44, App
83	25	34.7	9	US-10-161-097-45	Sequence 45, App
84	25	34.7	9	US-10-161-097-46	Sequence 46, App
85	25	34.7	9	US-10-161-097-47	Sequence 47, App
86	25	34.7	9	US-10-161-097-48	Sequence 48, App
87	25	34.7	9	US-10-161-097-49	Sequence 49, App
88	25	34.7	9	US-10-161-097-50	Sequence 50, App
89	25	34.7	9	US-10-161-097-51	Sequence 51, App
90	25	34.7	9	US-10-161-097-52	Sequence 52, App
91	25	34.7	9	US-10-161-097-53	Sequence 53, App
92	25	34.7	9	US-10-161-097-54	Sequence 54, App
93	25	34.7	9	US-10-161-097-55	Sequence 55, App
94	25	34.7	9	US-10-161-097-56	Sequence 56, App
95	25	34.7	9	US-10-161-097-57	Sequence 57, App
96	25	34.7	9	US-10-161-097-58	Sequence 58, App
97	25	34.7	9	US-10-161-097-59	Sequence 59, App
98	25	34.7	9	US-10-161-097-60	Sequence 60, App
99	25	34.7	9	US-10-161-097-61	Sequence 61, App
100	25	34.7	9	US-10-161-097-62	Sequence 62, App

101	25	34.7	9	4	US-10-685-977-87	Sequence 87, Appl	174	24	33.3	11	6	US-11-136-186-127	Sequence 127, App
102	25	34.7	9	4	US-10-685-977-88	Sequence 88, Appl	175	24	33.3	12	4	US-10-036-729-11	Sequence 10, Appl
103	25	34.7	9	4	US-10-685-977-89	Sequence 89, Appl	176	24	33.3	12	4	US-10-036-729-11	Sequence 11, Appl
104	25	34.7	9	4	US-10-685-977-90	Sequence 90, Appl	177	24	33.3	12	5	US-10-903-529-80	Sequence 80, Appl
105	25	34.7	9	4	US-10-685-977-91	Sequence 91, Appl	178	24	33.3	12	5	US-10-903-529-130	Sequence 130, Appl
106	25	34.7	9	4	US-10-685-977-92	Sequence 92, Appl	179	24	33.3	12	5	US-10-937-042-80	Sequence 80, Appl
107	25	34.7	9	4	US-10-685-977-93	Sequence 93, Appl	180	24	33.3	13	3	US-09-056-160B-60	Sequence 60, Appl
108	25	34.7	9	4	US-10-685-977-94	Sequence 94, Appl	181	24	33.3	13	4	US-10-120-604-129	Sequence 129, App
109	25	34.7	9	4	US-10-685-977-95	Sequence 95, Appl	182	24	33.3	13	4	US-10-234-607-18	Sequence 60, Appl
110	25	34.7	9	4	US-10-685-977-96	Sequence 96, Appl	183	24	33.3	13	4	US-10-652-407-8	Sequence 8, Appl
111	25	34.7	9	4	US-10-685-977-97	Sequence 97, Appl	184	24	33.3	13	5	US-10-974-591-60	Sequence 8, Appl
112	25	34.7	9	4	US-10-685-977-98	Sequence 98, Appl	185	24	33.3	13	5	US-10-517-707A-31	Sequence 31, Appl
113	25	34.7	9	4	US-10-685-977-99	Sequence 99, Appl	186	24	33.3	13	6	US-11-070-456-129	Sequence 129, App
114	25	34.7	9	4	US-10-685-977-100	Sequence 100, App	187	24	33.3	15	3	US-09-911-129B-14	Sequence 14, Appl
115	25	34.7	9	4	US-10-685-977-101	Sequence 101, App	188	24	33.3	15	4	US-10-652-407-63	Sequence 63, Appl
116	25	34.7	9	4	US-10-685-977-102	Sequence 102, App	189	24	33.3	15	4	US-10-795-795-14	Sequence 14, Appl
117	25	34.7	9	4	US-10-685-977-103	Sequence 103, App	190	24	33.3	15	4	US-10-795-795-14	Sequence 14, Appl
118	25	34.7	9	5	US-10-478-179-10	Sequence 10, App	191	24	33.3	15	5	US-10-517-707A-118	Sequence 118, App
119	25	34.7	9	5	US-10-362-715-5	Sequence 5, Appl	192	23	31.9	9	5	US-10-517-707A-119	Sequence 119, App
120	25	34.7	9	5	US-10-758-970-62	Sequence 62, Appl	193	23	31.9	9	5	US-10-884-862-307	Sequence 307, App
121	25	34.7	9	5	US-10-884-862-244	Sequence 244, App	194	23	31.9	10	3	US-09-572-270A-698	Sequence 698, App
122	25	34.7	9	5	US-10-705-459-42	Sequence 42, Appl	195	23	31.9	10	3	US-09-573-822C-13	Sequence 13, Appl
123	25	34.7	9	5	US-10-482-532-8	Sequence 8, Appl	196	23	31.9	10	4	US-10-026-066-51	Sequence 51, Appl
124	25	34.7	9	5	US-10-751-845-16	Sequence 16, Appl	197	23	31.9	10	4	US-10-327-598-702	Sequence 702, App
125	25	34.7	9	5	US-10-776-521B-363	Sequence 363, Appl	198	23	31.9	10	4	US-10-327-598-702	Sequence 703, App
126	25	34.7	9	5	US-10-820-067A-874	Sequence 874, Appl	199	23	31.9	10	4	US-10-327-598-710	Sequence 710, App
127	25	34.7	9	5	US-10-973-927-39	Sequence 39, Appl	200	23	31.9	10	4	US-10-658-180-33	Sequence 33, Appl
128	25	34.7	9	5	US-10-973-927-40	Sequence 40, Appl	201	23	31.9	10	4	US-10-658-180-33	Sequence 33, Appl
129	25	34.7	9	5	US-10-517-784-16	Sequence 16, Appl	202	23	31.9	10	5	US-10-956-401-24	Sequence 24, Appl
130	25	34.7	9	5	US-10-602-663-23	Sequence 23, Appl	203	23	31.9	10	5	US-10-895-523-51	Sequence 51, Appl
131	25	34.7	9	5	US-10-510-229-10	Sequence 10, Appl	204	23	31.9	11	6	US-10-530-061-1130	Sequence 1130, Ap
132	25	34.7	9	5	US-10-074-803-10	Sequence 10, Appl	205	23	31.9	11	6	US-11-051-453-78	Sequence 78, Appl
133	25	34.7	9	6	US-11-203-137-2	Sequence 2, Appl	206	23	31.9	12	3	US-09-828-708-38	Sequence 38, Appl
134	25	34.7	9	6	US-11-033-039-425	Sequence 25, App	207	23	31.9	12	3	US-09-828-708-40	Sequence 40, Appl
135	25	34.7	9	6	US-11-119-502-25	Sequence 25, Appl	208	23	31.9	12	3	US-09-828-708-41	Sequence 41, Appl
136	25	34.7	9	6	US-11-240-341-31	Sequence 31, Appl	209	23	31.9	12	3	US-09-828-708-42	Sequence 42, Appl
137	25	34.7	10	3	US-09-572-404B-211	Sequence 211, App	210	23	31.9	12	3	US-09-563-222-11	Sequence 11, Appl
138	25	34.7	10	3	US-09-898-860-49	Sequence 49, Appl	211	23	31.9	12	3	US-09-842-776A-19	Sequence 19, Appl
139	25	34.7	10	4	US-10-258-144-11	Sequence 11, Appl	212	23	31.9	12	4	US-10-001-934-62	Sequence 62, Appl
140	25	34.7	10	4	US-10-777-053-435	Sequence 435, App	213	23	31.9	12	4	US-10-190-082-410	Sequence 410, App
141	25	34.7	10	4	US-10-481-180-97	Sequence 97, Appl	214	23	31.9	12	4	US-10-286-457-65	Sequence 65, Appl
142	25	34.7	10	4	US-10-837-217-435	Sequence 435, App	215	23	31.9	12	4	US-10-374-932-8	Sequence 8, Appl
143	25	34.7	10	4	US-10-685-977-49	Sequence 49, Appl	216	23	31.9	12	4	US-10-338-366-20	Sequence 20, Appl
144	25	34.7	10	4	US-10-481-180-99	Sequence 99, Appl	217	23	31.9	12	4	US-10-275-046-19	Sequence 19, Appl
145	25	34.7	11	4	US-10-387-486-5	Sequence 5, Appl	218	23	31.9	12	4	US-10-601-837-23	Sequence 23, Appl
146	25	34.7	12	6	US-11-098-404-5	Sequence 25, Appl	219	23	31.9	12	4	US-10-379-741-8	Sequence 8, Appl
147	25	34.7	13	6	US-11-019-894A-25	Sequence 25, Appl	220	23	31.9	12	4	US-10-363-328A-2	Sequence 2, Appl
148	25	34.7	15	3	US-09-820-053A-152	Sequence 152, App	221	23	31.9	12	4	US-10-663-244-30	Sequence 30, Appl
149	25	34.7	15	4	US-10-109-171-152	Sequence 152, App	222	23	31.9	12	4	US-10-714-353-38	Sequence 38, Appl
150	25	34.7	15	4	US-10-416-413-6	Sequence 6, Appl	223	23	31.9	12	4	US-10-783-950-11	Sequence 11, Appl
151	25	34.7	15	5	US-10-839-525-152	Sequence 152, App	224	23	31.9	12	5	US-10-684-957-38	Sequence 38, Appl
152	25	34.7	15	5	US-11-136-186-152	Sequence 152, App	225	23	31.9	12	5	US-10-783-311-304	Sequence 304, App
153	25	34.7	15	6	US-11-045-024-12948	Sequence 12948, A	226	23	31.9	12	5	US-10-883-020-15	Sequence 15, Appl
154	25	34.7	15	6	US-10-052-578-11	Sequence 11, Appl	227	23	31.9	12	5	US-10-903-529-86	Sequence 86, Appl
155	25	34.7	8	4	US-10-053-520-11	Sequence 11, Appl	228	23	31.9	12	5	US-10-903-529-136	Sequence 136, App
156	25	34.7	8	4	US-10-053-498B-11	Sequence 11, Appl	229	23	31.9	12	5	US-10-726-332-146	Sequence 146, App
157	25	34.7	8	4	US-10-328-953-92	Sequence 92, Appl	230	23	31.9	12	5	US-10-726-332-158	Sequence 158, App
158	25	34.7	8	4	US-10-820-067A-402	Sequence 402, App	231	23	31.9	12	5	US-10-687-035-69	Sequence 69, Appl
159	25	34.7	9	3	US-09-935-682-22	Sequence 22, Appl	232	23	31.9	12	5	US-10-891-658-117	Sequence 117, App
160	25	34.7	9	5	US-10-119-536A-41	Sequence 41, Appl	233	23	31.9	12	5	US-10-891-658-113	Sequence 113, App
161	25	34.7	9	5	US-10-996-306-41	Sequence 41, Appl	234	23	31.9	12	5	US-10-891-658-113	Sequence 113, App
162	25	34.7	9	6	US-11-018-868-131	Sequence 131, Appl	235	23	31.9	12	5	US-10-891-658-113	Sequence 113, App
163	25	34.7	10	3	US-09-779-308-267	Sequence 267, App	236	23	31.9	12	5	US-10-630-009-125	Sequence 125, App
164	25	34.7	10	3	US-09-779-308-337	Sequence 337, App	237	23	31.9	12	5	US-10-630-009-41	Sequence 41, Appl
165	25	34.7	10	3	US-09-779-308-567	Sequence 567, App	238	23	31.9	12	5	US-10-630-009-41	Sequence 41, Appl
166	25	34.7	10	3	US-09-779-308-637	Sequence 637, App	239	23	31.9	12	5	US-10-630-009-42	Sequence 42, Appl
167	25	34.7	10	3	US-09-572-404B-1725	Sequence 1725, Ap	240	23	31.9	12	5	US-10-506-743-4	Sequence 4, Appl
168	25	34.7	10	3	US-09-573-822C-212	Sequence 212, App	241	23	31.9	12	5	US-10-982-725-8	Sequence 8, Appl
169	25	34.7	10	3	US-09-573-822C-481	Sequence 481, App	242	23	31.9	12	5	US-10-505-313-96	Sequence 96, Appl
170	25	34.7	11	3	US-09-820-053A-127	Sequence 127, App	243	23	31.9	12	5	US-10-505-313-143	Sequence 143, App
171	25	34.7	11	4	US-10-109-171-127	Sequence 127, App	244	23	31.9	12	5	US-10-505-313-211	Sequence 211, App
172	25	34.7	11	4	US-10-109-171-127	Sequence 127, App	245	23	31.9	12	5	US-10-989-462-79	Sequence 79, Appl
173	25	34.7	11	5	US-10-839-525-127	Sequence 127, App	246	23	31.9	12	5	US-10-507-662-12	Sequence 12, Appl

247	23	31.9	12	5	US-10-850-635-30	Sequence 30, Appl	320	22	30.6	10	4	US-10-481-180-776	Sequence 776, App
248	23	31.9	12	5	US-10-850-635-36	Sequence 36, Appl	321	22	30.6	10	4	US-10-243-795-972	Sequence 972, App
249	23	31.9	12	5	US-10-880-238-84	Sequence 84, Appl	322	22	30.6	10	4	US-10-243-795-1635	Sequence 1635, App
250	23	31.9	12	5	US-10-880-238-87	Sequence 87, Appl	323	22	30.6	10	5	US-10-474-860A-266	Sequence 266, App
251	23	31.9	12	5	US-10-880-238-90	Sequence 90, Appl	324	22	30.6	10	5	US-10-846-548A-6	Sequence 6, Appl
252	23	31.9	12	5	US-10-880-238-93	Sequence 93, Appl	325	22	30.6	10	6	US-11-029-331-43	Sequence 43, Appl
253	23	31.9	12	5	US-10-880-238-96	Sequence 96, Appl	326	22	30.6	10	6	US-11-045-024-81	Sequence 81, Appl
254	23	31.9	12	5	US-10-880-238-99	Sequence 99, Appl	327	22	30.6	10	6	US-11-045-024-6100	Sequence 6100, App
255	23	31.9	12	5	US-10-880-238-102	Sequence 102, App	328	22	30.6	11	4	US-10-481-180-875	Sequence 785, App
256	23	31.9	12	5	US-10-880-238-105	Sequence 105, App	329	22	30.6	11	5	US-10-808-187-1620	Sequence 1620, App
257	23	31.9	12	6	US-11-009-731-53	Sequence 53, App	330	22	30.6	11	5	US-10-807-807-1620	Sequence 1620, App
258	23	31.9	12	6	US-11-009-731-55	Sequence 55, Appl	331	22	30.6	11	6	US-11-004-399-2313	Sequence 2313, App
259	23	31.9	12	6	US-11-009-731-60	Sequence 60, Appl	332	22	30.6	12	3	US-09-977-797A-24	Sequence 24, Appl
260	23	31.9	12	6	US-11-009-731-61	Sequence 61, Appl	333	22	30.6	12	4	US-10-312-116-23	Sequence 23, Appl
261	23	31.9	12	6	US-11-051-453-68	Sequence 68, Appl	334	22	30.6	12	4	US-10-481-180-790	Sequence 790, App
262	23	31.9	13	3	US-09-876-904A-156	Sequence 156, App	335	22	30.6	12	4	US-10-738-120-16	Sequence 16, Appl
263	23	31.9	13	5	US-10-511-559-254	Sequence 254, App	336	22	30.6	12	5	US-10-783-311-112	Sequence 112, App
264	23	31.9	13	5	US-10-511-559-333	Sequence 333, App	337	22	30.6	13	3	US-09-935-682-54	Sequence 54, Appl
265	23	31.9	13	5	US-10-511-559-334	Sequence 334, App	338	22	30.6	13	4	US-10-281-478-50	Sequence 50, Appl
266	23	31.9	14	5	US-10-846-188C-5	Sequence 5, Appl	339	22	30.6	13	4	US-10-174-613-30	Sequence 30, Appl
267	23	31.9	14	6	US-11-066-697-1409	Sequence 1409, App	340	22	30.6	13	4	US-10-116-519-30	Sequence 30, Appl
268	23	31.9	15	4	US-10-229-567-23	Sequence 23, Appl	341	22	30.6	13	4	US-10-116-519-59	Sequence 59, Appl
269	23	31.9	15	4	US-10-149-137A-9	Sequence 9, Appl	342	22	30.6	13	4	US-10-116-519-78	Sequence 78, Appl
270	23	31.9	15	4	US-10-149-137A-101	Sequence 101, App	343	22	30.6	13	4	US-10-336-753-75	Sequence 75, Appl
271	23	31.9	15	5	US-10-489-802-27	Sequence 27, Appl	344	22	30.6	13	4	US-10-308-128-33	Sequence 33, Appl
272	23	31.9	15	5	US-10-769-514-84	Sequence 84, Appl	345	22	30.6	13	5	US-10-517-707A-310	Sequence 30, Appl
273	23	31.9	15	5	US-10-622-003-10	Sequence 10, Appl	346	22	30.6	13	6	US-11-033-039-1413	Sequence 1413, App
274	23	31.9	15	5	US-10-801-890-344	Sequence 344, App	347	22	30.6	14	4	US-10-174-613-41	Sequence 41, Appl
275	23	31.9	15	5	US-10-776-224-130	Sequence 130, App	348	22	30.6	14	4	US-10-808-128-42	Sequence 42, Appl
276	23	31.9	15	5	US-10-715-810-14	Sequence 14, Appl	349	22	30.6	14	5	US-10-813-338-1458	Sequence 1458, App
277	23	31.9	15	5	US-10-715-810-29	Sequence 29, Appl	350	22	30.6	14	5	US-10-946-647-1025	Sequence 1025, App
278	23	31.9	15	5	US-10-715-810-86	Sequence 86, Appl	351	22	30.6	14	5	US-10-946-647-1181	Sequence 1181, App
279	23	31.9	15	5	US-10-525-113-23	Sequence 23, Appl	352	22	30.6	15	3	US-09-908-943A-42	Sequence 42, Appl
280	23	31.9	15	5	US-10-530-061-1698	Sequence 1698, App	353	22	30.6	15	4	US-10-294-891-27	Sequence 27, Appl
281	23	31.9	15	5	US-10-530-061-1699	Sequence 1699, App	354	22	30.6	15	4	US-10-149-138-3742	Sequence 3742, App
282	23	31.9	15	5	US-10-530-061-1710	Sequence 1710, App	355	22	30.6	15	4	US-10-149-138-3846	Sequence 3846, App
283	23	31.9	15	5	US-10-530-061-1880	Sequence 1880, App	356	22	30.6	15	4	US-10-676-909-28	Sequence 28, Appl
284	23	31.9	15	6	US-11-105-725-5	Sequence 5, Appl	357	22	30.6	15	4	US-10-149-138-3742	Sequence 3742, App
285	23	31.9	15	6	US-11-045-024-12916	Sequence 12916, A	358	22	30.6	15	4	US-10-149-138-3846	Sequence 3846, App
286	23	31.9	15	6	US-11-045-024-12972	Sequence 12972, A	359	22	30.6	15	5	US-10-801-487-42	Sequence 42, Appl
287	22	30.6	6	4	US-10-328-953-45	Sequence 45, Appl	360	22	30.6	15	5	US-10-801-538-42	Sequence 42, Appl
288	22	30.6	6	4	US-10-367-580-315	Sequence 315, App	361	22	30.6	15	5	US-10-801-509-42	Sequence 42, Appl
289	22	30.6	6	4	US-10-367-593-315	Sequence 315, App	362	22	30.6	15	5	US-10-801-486-42	Sequence 42, Appl
290	22	30.6	6	4	US-10-367-594-315	Sequence 315, App	363	22	30.6	15	5	US-10-788-992-13	Sequence 13, Appl
291	22	30.6	6	4	US-10-367-654-315	Sequence 315, App	364	22	30.6	15	5	US-10-920-313-27	Sequence 27, Appl
292	22	30.6	6	4	US-10-367-658-315	Sequence 315, App	365	22	30.6	15	5	US-10-471-894B-127	Sequence 127, App
293	22	30.6	6	4	US-10-367-658-315	Sequence 315, App	366	22	30.6	15	5	US-10-801-493-42	Sequence 42, Appl
294	22	30.6	6	4	US-10-367-674-315	Sequence 315, App	367	22	30.6	15	5	US-10-902-886-37	Sequence 37, Appl
295	22	30.6	6	5	US-10-820-067A-297	Sequence 297, App	368	22	30.6	15	6	US-11-009-460-37	Sequence 37, Appl
296	22	30.6	8	4	US-10-050-271-3	Sequence 3, Appl	369	22	30.6	15	6	US-11-066-697-1244	Sequence 1244, App
297	22	30.6	8	5	US-10-958-216-1000	Sequence 1000, App	370	22	30.6	15	6	US-11-064-039-15	Sequence 15, Appl
298	22	30.6	8	6	US-11-064-416-3	Sequence 3, Appl	371	22	30.6	15	6	US-11-065-970-57	Sequence 57, Appl
299	22	30.6	9	2	US-08-452-843A-9	Sequence 9, Appl	372	22	30.6	15	6	US-11-045-024-12926	Sequence 12926, A
300	22	30.6	9	4	US-10-219-850-9	Sequence 9, Appl	373	22	30.6	15	6	US-11-167-636-57	Sequence 57, Appl
301	22	30.6	9	4	US-10-353-678-15	Sequence 15, Appl	374	21	29.2	7	4	US-10-548-748-52	Sequence 52, Appl
302	22	30.6	9	4	US-10-149-138-2761	Sequence 2761, App	375	21	29.2	7	4	US-10-397-062-26	Sequence 26, Appl
303	22	30.6	9	4	US-10-149-138-3384	Sequence 3384, App	376	21	29.2	7	5	US-10-928-312-3	Sequence 3, Appl
304	22	30.6	9	4	US-10-149-138-2761	Sequence 2761, App	377	21	29.2	7	5	US-10-937-042-146	Sequence 146, App
305	22	30.6	9	4	US-10-149-138-3384	Sequence 3384, App	378	21	29.2	7	5	US-10-885-788A-454	Sequence 454, App
306	22	30.6	9	4	US-10-364-645A-5	Sequence 5, Appl	379	21	29.2	8	3	US-10-548-748-53	Sequence 53, Appl
307	22	30.6	9	4	US-10-364-645A-36	Sequence 36, Appl	380	21	29.2	8	3	US-09-756-283A-88	Sequence 88, Appl
308	22	30.6	9	5	US-10-808-187-1408	Sequence 1408, App	381	21	29.2	8	4	US-10-014-340-226	Sequence 226, App
309	22	30.6	9	5	US-10-807-807-1408	Sequence 1408, App	382	21	29.2	8	4	US-10-105-735-25	Sequence 25, Appl
310	22	30.6	9	5	US-10-530-061-897	Sequence 897, App	383	21	29.2	8	4	US-10-050-271-4	Sequence 4, Appl
311	22	30.6	9	5	US-10-530-061-992	Sequence 992, App	384	21	29.2	8	4	US-10-753-881-88	Sequence 88, Appl
312	22	30.6	9	5	US-10-530-061-1102	Sequence 1102, App	385	21	29.2	8	4	US-10-486-090-1	Sequence 1, Appl
313	22	30.6	9	6	US-11-045-024-57	Sequence 57, Appl	386	21	29.2	8	5	US-10-903-529-79	Sequence 79, Appl
314	22	30.6	9	6	US-11-045-024-3803	Sequence 3803, App	387	21	29.2	8	5	US-10-903-529-129	Sequence 129, App
315	22	30.6	9	6	US-11-045-024-6944	Sequence 6944, App	388	21	29.2	8	5	US-10-654-601-1240	Sequence 1240, App
316	22	30.6	9	6	US-11-026-403-15	Sequence 15, Appl	389	21	29.2	8	5	US-10-654-601-1370	Sequence 1370, App
317	22	30.6	9	6	US-11-004-399-2101	Sequence 2101, App	390	21	29.2	8	5	US-10-937-042-79	Sequence 79, Appl
318	22	30.6	10	3	US-09-894-018-266	Sequence 266, App	391	21	29.2	8	5	US-10-485-788A-455	Sequence 455, App
319	22	30.6	10	4	US-10-137-867-204	Sequence 204, App	392	21	29.2	8	6	US-11-105-725-8	Sequence 8, Appl

393	21	29.2	8	US-11-051-411-424	Sequence 424, App	466	21	29.2	10	US-10-990-137-162	Sequence 162, App
394	21	29.2	8	US-11-051-411-627	Sequence 627, App	467	21	29.2	10	US-10-990-137-262	Sequence 262, App
395	21	29.2	8	US-11-045-024-129	Sequence 129, App	468	21	29.2	10	US-10-990-137-400	Sequence 400, App
396	21	29.2	8	US-11-045-024-4052	Sequence 4052, App	469	21	29.2	10	US-10-989-767A-162	Sequence 162, App
397	21	29.2	8	US-11-045-024-6334	Sequence 6334, App	470	21	29.2	10	US-10-989-767A-262	Sequence 262, App
398	21	29.2	8	US-11-045-024-6354	Sequence 6354, App	471	21	29.2	10	US-10-989-767A-420	Sequence 420, App
399	21	29.2	8	US-11-045-024-8965	Sequence 8965, App	472	21	29.2	10	US-11-105-725-9	Sequence 9, App1
400	21	29.2	8	US-11-045-024-9005	Sequence 9005, App	473	21	29.2	10	US-11-051-411-8	Sequence 8, App1
401	21	29.2	8	US-11-064-416-4	Sequence 4, App1	474	21	29.2	10	US-11-051-411-292	Sequence 292, App
402	21	29.2	9	US-09-821-819A-4	Sequence 4, App1	475	21	29.2	10	US-11-051-411-482	Sequence 482, App
403	21	29.2	9	US-09-894-018-311	Sequence 311, App	476	21	29.2	10	US-11-051-411-631	Sequence 631, App
404	21	29.2	9	US-09-779-308-413	Sequence 413, App	477	21	29.2	10	US-11-051-411-715	Sequence 715, App
405	21	29.2	9	US-09-898-860-124	Sequence 124, App	478	21	29.2	10	US-11-051-411-924	Sequence 924, App
406	21	29.2	9	US-10-215-272-43	Sequence 43, App1	479	21	29.2	10	US-11-000-328-27	Sequence 27, App1
407	21	29.2	9	US-10-716-326-43	Sequence 43, App1	480	21	29.2	10	US-11-045-024-5229	Sequence 5229, App
408	21	29.2	9	US-10-685-977-124	Sequence 124, App	481	21	29.2	10	US-11-045-024-5231	Sequence 5231, App
409	21	29.2	9	US-10-474-960A-311	Sequence 311, App	482	21	29.2	10	US-11-045-024-5233	Sequence 5233, App
410	21	29.2	9	US-10-275-652-59	Sequence 59, App1	483	21	29.2	10	US-11-045-024-5234	Sequence 5234, App
411	21	29.2	9	US-10-894-834-4	Sequence 4, App1	484	21	29.2	10	US-11-045-024-7199	Sequence 7199, App
412	21	29.2	9	US-10-930-300-31	Sequence 31, App1	485	21	29.2	10	US-11-045-024-7205	Sequence 7205, App
413	21	29.2	9	US-10-884-862-6	Sequence 6, App1	486	21	29.2	10	US-11-045-024-7205	Sequence 7205, App
414	21	29.2	9	US-10-715-976-43	Sequence 43, App1	487	21	29.2	10	US-11-045-024-7207	Sequence 7207, App
415	21	29.2	9	US-10-530-061-615	Sequence 615, App	488	21	29.2	10	US-11-130-206-26	Sequence 26, App1
416	21	29.2	9	US-11-051-411-534	Sequence 534, App	489	21	29.2	10	US-11-130-206-34	Sequence 34, App1
417	21	29.2	9	US-11-051-411-841	Sequence 841, App	490	21	29.2	10	US-11-130-206-42	Sequence 42, App1
418	21	29.2	9	US-11-051-411-1015	Sequence 1015, App	491	21	29.2	11	US-09-966-871-70	Sequence 70, App1
419	21	29.2	9	US-11-045-024-150	Sequence 150, App	492	21	29.2	11	US-09-908-943A-122	Sequence 122, App
420	21	29.2	9	US-11-045-024-151	Sequence 151, App	493	21	29.2	11	US-10-039-645-70	Sequence 70, App1
421	21	29.2	9	US-11-045-024-4119	Sequence 4119, App	494	21	29.2	11	US-10-139-084-70	Sequence 70, App1
422	21	29.2	9	US-11-045-024-4120	Sequence 4120, App	495	21	29.2	11	US-10-083-259-149	Sequence 149, App
423	21	29.2	9	US-11-045-024-7244	Sequence 7244, App	496	21	29.2	11	US-10-083-259-150	Sequence 150, App
424	21	29.2	9	US-11-045-024-7267	Sequence 7267, App	497	21	29.2	11	US-10-109-274A-149	Sequence 149, App
425	21	29.2	9	US-11-045-024-8939	Sequence 8939, App	498	21	29.2	11	US-10-109-274A-150	Sequence 150, App
426	21	29.2	9	US-11-045-024-9014	Sequence 9014, App	499	21	29.2	11	US-10-458-860-70	Sequence 70, App1
427	21	29.2	9	US-11-045-024-13722	Sequence 13722, App	500	21	29.2	11	US-10-801-481-122	Sequence 122, App
428	21	29.2	9	US-11-045-024-13734	Sequence 13734, App	501	21	29.2	11	US-10-801-938-122	Sequence 122, App
429	21	29.2	9	US-11-146-854-43	Sequence 43, App1	502	21	29.2	11	US-10-801-938-122	Sequence 122, App
430	21	29.2	10	US-11-129-741-3471	Sequence 3471, App	503	21	29.2	11	US-10-801-938-122	Sequence 122, App
431	21	29.2	10	US-09-935-430-162	Sequence 162, App	504	21	29.2	11	US-10-801-938-122	Sequence 122, App
432	21	29.2	10	US-09-935-430-262	Sequence 262, App	505	21	29.2	11	US-10-654-601-241	Sequence 241, App
433	21	29.2	10	US-09-935-430-262	Sequence 262, App	506	21	29.2	11	US-10-654-601-510	Sequence 510, App
434	21	29.2	10	US-09-572-404B-3147	Sequence 3147, App	507	21	29.2	11	US-10-654-601-1030	Sequence 1030, App
435	21	29.2	10	US-09-572-270A-428	Sequence 428, App	508	21	29.2	11	US-10-654-601-1371	Sequence 1371, App
436	21	29.2	10	US-09-896-923-8	Sequence 8, App1	509	21	29.2	11	US-10-801-493-122	Sequence 122, App
437	21	29.2	10	US-10-116-255-39	Sequence 39, App1	510	21	29.2	11	US-10-773-274A-28	Sequence 28, App1
438	21	29.2	10	US-10-062-710-41	Sequence 41, App1	511	21	29.2	11	US-10-530-061-783	Sequence 783, App
439	21	29.2	10	US-10-277-292-162	Sequence 162, App	512	21	29.2	11	US-11-022-327-5	Sequence 5, App1
440	21	29.2	10	US-10-277-292-262	Sequence 262, App	513	21	29.2	11	US-11-022-327-16	Sequence 16, App1
441	21	29.2	10	US-10-277-292-420	Sequence 420, App	514	21	29.2	11	US-11-022-327-54	Sequence 54, App1
442	21	29.2	10	US-10-280-340-162	Sequence 162, App	515	21	29.2	11	US-11-051-411-821	Sequence 821, App
443	21	29.2	10	US-10-280-340-262	Sequence 262, App	516	21	29.2	11	US-11-045-024-1472	Sequence 1472, App
444	21	29.2	10	US-10-280-340-420	Sequence 420, App	517	21	29.2	11	US-11-045-024-4223	Sequence 4223, App
445	21	29.2	10	US-10-442-909-12	Sequence 12, App1	518	21	29.2	11	US-11-045-024-4223	Sequence 4223, App
446	21	29.2	10	US-10-223-650-8	Sequence 8, App1	519	21	29.2	11	US-11-045-024-12606	Sequence 12606, App
447	21	29.2	10	US-10-376-647B-33	Sequence 33, App1	520	21	29.2	12	US-09-948-939-24	Sequence 24, App1
448	21	29.2	10	US-10-351-608A-33	Sequence 33, App1	521	21	29.2	12	US-09-908-943A-11	Sequence 11, App1
449	21	29.2	10	US-10-741-204-45	Sequence 45, App1	522	21	29.2	12	US-09-908-943A-121	Sequence 121, App1
450	21	29.2	10	US-10-432-234A-448	Sequence 448, App	523	21	29.2	12	US-09-956-940-5	Sequence 5, App1
451	21	29.2	10	US-10-432-234A-449	Sequence 449, App	524	21	29.2	12	US-09-956-940-26	Sequence 26, App1
452	21	29.2	10	US-10-432-234A-450	Sequence 450, App	525	21	29.2	12	US-09-820-053A-67	Sequence 67, App1
453	21	29.2	10	US-10-432-234A-451	Sequence 451, App	526	21	29.2	12	US-09-954-385-382	Sequence 382, App
454	21	29.2	10	US-10-432-234A-452	Sequence 452, App	527	21	29.2	12	US-09-747-287-45	Sequence 45, App1
455	21	29.2	10	US-10-432-234A-453	Sequence 453, App	528	21	29.2	12	US-09-874-350A-11	Sequence 11, App1
456	21	29.2	10	US-10-481-180-329	Sequence 329, App	529	21	29.2	12	US-10-033-741-41	Sequence 41, App1
457	21	29.2	10	US-10-693-331-27	Sequence 27, App1	530	21	29.2	12	US-10-033-662-41	Sequence 41, App1
458	21	29.2	10	US-10-780-321-38	Sequence 38, App1	531	21	29.2	12	US-10-109-171-67	Sequence 67, App1
459	21	29.2	10	US-10-833-951-201	Sequence 201, App	532	21	29.2	12	US-10-237-852-26	Sequence 26, App1
460	21	29.2	10	US-10-654-601-298	Sequence 498, App	533	21	29.2	12	US-10-083-259-154	Sequence 154, App
461	21	29.2	10	US-10-654-601-1021	Sequence 1021, App	534	21	29.2	12	US-10-083-259-156	Sequence 156, App
462	21	29.2	10	US-10-654-601-1163	Sequence 1163, App	535	21	29.2	12	US-10-109-274A-154	Sequence 154, App
463	21	29.2	10	US-10-936-237-14	Sequence 14, App1	536	21	29.2	12	US-10-109-274A-156	Sequence 156, App
464	21	29.2	10	US-10-839-456-8	Sequence 8, App1	537	21	29.2	12	US-10-038-854-213	Sequence 213, App
465	21	29.2	10	US-10-773-274A-27	Sequence 27, App1	538	21	29.2	12	US-10-431-596-80	Sequence 80, App1

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540	21	29.2	12	5	US-10-839-525-67	Sequence 67, Appl	613	21	29.2	14	5	US-10-807-807-1835	Sequence 1835, Ap
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542	21	29.2	12	5	US-10-801-487-121	Sequence 121, Appl	615	21	29.2	14	5	US-10-895-064-1505	Sequence 1505, Ap
543	21	29.2	12	5	US-10-801-938-41	Sequence 41, Appl	616	21	29.2	14	5	US-10-530-061-1907	Sequence 1907, Ap
544	21	29.2	12	5	US-10-801-938-121	Sequence 121, Appl	617	21	29.2	14	5	US-10-530-061-1908	Sequence 1908, Ap
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547	21	29.2	12	5	US-10-801-486-41	Sequence 41, Appl	620	21	29.2	14	6	US-11-129-741-3536	Sequence 3536, Ap
548	21	29.2	12	5	US-10-801-486-121	Sequence 121, Appl	621	21	29.2	14	6	US-11-004-499-2528	Sequence 2528, Ap
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550	21	29.2	12	5	US-10-803-738-16	Sequence 16, Appl	623	21	29.2	15	3	US-09-160-076-2	Sequence 2, Appl
551	21	29.2	12	5	US-10-912-512-382	Sequence 382, Appl	624	21	29.2	15	3	US-09-947-770-21	Sequence 21, Appl
552	21	29.2	12	5	US-10-935-642-54	Sequence 54, Appl	625	21	29.2	15	3	US-09-957-674-16	Sequence 16, Appl
553	21	29.2	12	5	US-10-726-332-161	Sequence 161, Appl	626	21	29.2	15	3	US-09-820-053A-43	Sequence 43, Appl
554	21	29.2	12	5	US-10-235-043-382	Sequence 382, Appl	627	21	29.2	15	4	US-10-015-536-24	Sequence 24, Appl
555	21	29.2	12	5	US-10-380-926-2	Sequence 2, Appl	628	21	29.2	15	4	US-10-174-105A-191	Sequence 191, Appl
556	21	29.2	12	5	US-10-493-41	Sequence 41, Appl	629	21	29.2	15	4	US-10-001-469-2511	Sequence 2511, Ap
557	21	29.2	12	5	US-10-801-493-121	Sequence 121, Appl	630	21	29.2	15	4	US-10-001-469-2539	Sequence 2539, Ap
558	21	29.2	12	5	US-10-937-042-86	Sequence 86, Appl	631	21	29.2	15	4	US-10-001-469-2576	Sequence 2576, Ap
559	21	29.2	12	6	US-10-773-274A-29	Sequence 29, Appl	632	21	29.2	15	4	US-10-001-469-2605	Sequence 2605, Ap
560	21	29.2	12	6	US-11-040-846-24	Sequence 24, Appl	633	21	29.2	15	4	US-10-001-469-2685	Sequence 2685, Ap
561	21	29.2	12	6	US-11-136-186-67	Sequence 67, Appl	634	21	29.2	15	4	US-10-001-469-2686	Sequence 2686, Ap
562	21	29.2	12	6	US-11-074-473-54	Sequence 54, Appl	635	21	29.2	15	4	US-10-001-469-2747	Sequence 2747, Ap
563	21	29.2	13	3	US-09-820-053A-35	Sequence 35, Appl	636	21	29.2	15	4	US-10-001-469-2844	Sequence 2844, Ap
564	21	29.2	13	3	US-09-820-053A-157	Sequence 157, Appl	637	21	29.2	15	4	US-10-109-171-43	Sequence 43, Appl
565	21	29.2	13	3	US-09-848-107-7	Sequence 7, Appl	638	21	29.2	15	4	US-10-202-824-21	Sequence 21, Appl
566	21	29.2	13	4	US-10-109-171-35	Sequence 35, Appl	639	21	29.2	15	4	US-10-442-909-46	Sequence 46, Appl
567	21	29.2	13	4	US-10-109-171-157	Sequence 157, Appl	640	21	29.2	15	4	US-10-430-685-112	Sequence 112, Appl
568	21	29.2	13	4	US-10-372-076-152	Sequence 152, Appl	641	21	29.2	15	4	US-10-339-160-2	Sequence 2, Appl
569	21	29.2	13	4	US-10-264-309-308	Sequence 308, Appl	642	21	29.2	15	4	US-10-676-909-60	Sequence 60, Appl
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572	21	29.2	13	4	US-10-473-633-9	Sequence 9, Appl	645	21	29.2	15	5	US-10-839-525-43	Sequence 43, Appl
573	21	29.2	13	4	US-10-380-927-2	Sequence 2, Appl	646	21	29.2	15	5	US-10-476-104-35	Sequence 35, Appl
574	21	29.2	13	4	US-10-732-862A-165	Sequence 169, Appl	647	21	29.2	15	5	US-10-622-003-2	Sequence 2, Appl
575	21	29.2	13	4	US-10-677-074-152	Sequence 152, Appl	648	21	29.2	15	5	US-10-622-003-4	Sequence 4, Appl
576	21	29.2	13	5	US-10-839-525-35	Sequence 35, Appl	649	21	29.2	15	5	US-10-622-003-13	Sequence 13, Appl
577	21	29.2	13	5	US-10-839-525-157	Sequence 157, Appl	650	21	29.2	15	5	US-10-471-894B-102	Sequence 102, Appl
578	21	29.2	13	5	US-10-801-990-311	Sequence 311, Appl	651	21	29.2	15	5	US-10-471-894B-103	Sequence 103, Appl
579	21	29.2	13	5	US-10-471-894B-26	Sequence 26, Appl	652	21	29.2	15	5	US-10-654-601-2080	Sequence 2080, Ap
580	21	29.2	13	5	US-10-471-894B-27	Sequence 27, Appl	653	21	29.2	15	5	US-10-654-601-2083	Sequence 2083, Ap
581	21	29.2	13	5	US-10-264-309-308	Sequence 308, Appl	654	21	29.2	15	5	US-10-654-601-2215	Sequence 2215, Ap
582	21	29.2	13	5	US-10-937-042-147	Sequence 147, Appl	655	21	29.2	15	5	US-10-660-370-12	Sequence 12, Appl
583	21	29.2	13	5	US-10-773-274A-30	Sequence 30, Appl	656	21	29.2	15	5	US-10-660-370-53	Sequence 53, Appl
584	21	29.2	13	5	US-10-948-707-686	Sequence 686, Appl	657	21	29.2	15	5	US-10-660-370-80	Sequence 80, Appl
585	21	29.2	13	5	US-10-948-707-912	Sequence 912, Appl	658	21	29.2	15	5	US-10-656-250-102	Sequence 102, Appl
586	21	29.2	13	5	US-10-948-707-938	Sequence 938, Appl	659	21	29.2	15	5	US-10-862-195-1354	Sequence 1354, Ap
587	21	29.2	13	5	US-10-948-707-1021	Sequence 1021, Ap	660	21	29.2	15	5	US-10-862-195-1361	Sequence 1361, Ap
588	21	29.2	13	5	US-10-948-707-1290	Sequence 1290, Ap	661	21	29.2	15	5	US-10-773-274A-32	Sequence 32, Appl
589	21	29.2	13	5	US-10-948-707-1330	Sequence 1330, Ap	662	21	29.2	15	5	US-10-958-216-669	Sequence 669, Appl
590	21	29.2	13	5	US-10-948-707-1335	Sequence 1335, Ap	663	21	29.2	15	5	US-10-946-647-1292	Sequence 1292, Ap
591	21	29.2	13	5	US-10-511-559-682	Sequence 682, Appl	664	21	29.2	15	5	US-10-511-559-75	Sequence 75, Appl
592	21	29.2	13	5	US-10-511-559-683	Sequence 683, Appl	665	21	29.2	15	5	US-10-530-061-1461	Sequence 1461, Ap
593	21	29.2	13	5	US-10-511-559-684	Sequence 684, Appl	666	21	29.2	15	5	US-10-530-061-1462	Sequence 1462, Ap
594	21	29.2	13	5	US-10-511-559-685	Sequence 685, Appl	667	21	29.2	15	5	US-10-530-061-1463	Sequence 1463, Ap
595	21	29.2	13	5	US-10-511-559-686	Sequence 686, Appl	668	21	29.2	15	5	US-10-530-061-1464	Sequence 1464, Ap
596	21	29.2	13	5	US-10-511-559-910	Sequence 910, Appl	669	21	29.2	15	5	US-10-530-061-1465	Sequence 1465, Ap
597	21	29.2	13	5	US-10-511-559-911	Sequence 911, Appl	670	21	29.2	15	5	US-10-530-061-1677	Sequence 1677, Ap
598	21	29.2	13	6	US-11-111-072-7	Sequence 7, Appl	671	21	29.2	15	5	US-10-530-061-1678	Sequence 1678, Ap
599	21	29.2	13	6	US-11-136-186-35	Sequence 35, Appl	672	21	29.2	15	5	US-10-530-061-1867	Sequence 1867, Ap
600	21	29.2	13	6	US-11-136-186-157	Sequence 157, Appl	673	21	29.2	15	5	US-10-530-061-1904	Sequence 1904, Ap
601	21	29.2	14	3	US-09-922-261-391	Sequence 391, Appl	674	21	29.2	15	5	US-10-530-061-1905	Sequence 1905, Ap
602	21	29.2	14	3	US-09-116-676-4	Sequence 4, Appl	675	21	29.2	15	5	US-10-530-061-1913	Sequence 1913, Ap
603	21	29.2	14	4	US-10-432-422-97	Sequence 97, Appl	676	21	29.2	15	5	US-10-530-061-1915	Sequence 1915, Ap
604	21	29.2	14	4	US-10-676-909-59	Sequence 59, Appl	677	21	29.2	15	5	US-10-530-061-1916	Sequence 1916, Ap
605	21	29.2	14	4	US-10-475-104-87	Sequence 87, Appl	678	21	29.2	15	5	US-10-530-061-1917	Sequence 1917, Ap
606	21	29.2	14	4	US-10-746-547-9	Sequence 9, Appl	679	21	29.2	15	5	US-10-530-061-1921	Sequence 1921, Ap
607	21	29.2	14	5	US-10-808-187-1835	Sequence 1835, Ap	680	21	29.2	15	5	US-10-530-061-1922	Sequence 1922, Ap
608	21	29.2	14	5	US-10-869-040-138	Sequence 138, Appl	681	21	29.2	15	5	US-10-530-061-1923	Sequence 1923, Ap
609	21	29.2	14	5	US-10-860-370-449	Sequence 449, Appl	682	21	29.2	15	5	US-10-530-061-1924	Sequence 1924, Ap
610	21	29.2	14	5	US-10-660-370-474	Sequence 474, Appl	683	21	29.2	15	5	US-10-530-061-1925	Sequence 1925, Ap
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685 21 29.2 15 6 US-11-009-460-13 Sequence 13, Appl
686 21 29.2 15 6 US-11-009-460-104 Sequence 104, App
687 21 29.2 15 6 US-11-051-411-1057 Sequence 1057, Ap
688 21 29.2 15 6 US-11-136-186-43 Sequence 43, Appl
689 21 29.2 15 6 US-11-069-543-163 Sequence 163, App
690 21 29.2 15 6 US-11-136-464-21 Sequence 21, Appl
691 21 29.2 15 6 US-11-032-794-5 Sequence 5, Appl1
692 21 29.2 15 6 US-11-000-365-5 Sequence 13078, A
693 21 29.2 15 6 US-11-045-024-12973 Sequence 12973, A
694 21 29.2 15 6 US-11-045-024-13066 Sequence 13066, A
695 21 29.2 15 6 US-11-045-024-13078 Sequence 13078, A
696 21 29.2 15 6 US-11-045-024-13087 Sequence 13087, A
697 21 29.2 15 6 US-11-045-024-13090 Sequence 13090, A
698 21 29.2 15 6 US-11-206-679-2 Sequence 21, Appl1
699 21 29.2 15 6 US-11-289-226-21 Sequence 21, Appl
700 21 29.2 15 6 US-10-310-674A-20 Sequence 20, Appl
701 21 29.2 15 6 US-09-529-759-26 Sequence 26, Appl
702 21 29.2 15 6 US-10-310-674A-3 Sequence 3, Appl1
703 21 29.2 15 6 US-10-310-674A-22 Sequence 22, Appl
704 21 29.2 15 6 US-10-310-674A-19 Sequence 19, Appl
705 21 29.2 15 6 US-10-633-771-26 Sequence 26, Appl
706 21 29.2 15 6 US-11-104-353-26 Sequence 26, Appl
707 21 29.2 15 6 US-10-310-674A-23 Sequence 23, Appl
708 21 29.2 15 6 US-10-862-195-165 Sequence 166, App
709 21 29.2 15 6 US-09-982-172-202 Sequence 202, App
710 21 29.2 15 6 US-09-910-552-17 Sequence 17, Appl
711 21 29.2 15 6 US-10-042-202-42 Sequence 42, Appl
712 21 29.2 15 6 US-10-128-711-19 Sequence 19, Appl
713 21 29.2 15 6 US-10-079-167-2 Sequence 2, Appl1
714 21 29.2 15 6 US-10-079-167-22 Sequence 22, Appl
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716 21 29.2 15 6 US-10-149-138-2760 Sequence 2760, Ap
717 21 29.2 15 6 US-10-367-580-131 Sequence 131, App
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726 21 29.2 15 6 US-10-653-624-22 Sequence 22, Appl1
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734 21 29.2 15 6 US-10-833-744-22 Sequence 22, Appl1
735 21 29.2 15 6 US-10-686-943-2 Sequence 2, Appl1
736 21 29.2 15 6 US-10-686-943-22 Sequence 22, Appl1
737 21 29.2 15 6 US-10-946-647-346 Sequence 346, App
738 21 29.2 15 6 US-10-946-647-621 Sequence 621, App
739 21 29.2 15 6 US-10-776-521B-110 Sequence 110, App
740 21 29.2 15 6 US-10-820-067A-110 Sequence 110, App
741 21 29.2 15 6 US-11-045-024-8213 Sequence 8213, Ap
742 21 29.2 15 6 US-11-244-209-17 Sequence 17, Appl
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747 21 29.2 15 6 US-09-779-308-577 Sequence 577, App
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751 21 29.2 15 6 US-09-865-548A-304 Sequence 204, App
752 21 29.2 15 6 US-09-898-860-67 Sequence 67, Appl
753 21 29.2 15 6 US-10-094-699-67 Sequence 67, Appl
754 21 29.2 15 6 US-10-172-597-187 Sequence 187, App
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756 21 29.2 15 6 US-10-280-340-560 Sequence 560, App
757 21 29.2 15 6 US-10-334-726-109 Sequence 109, App
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758 20 27.8 9 4 US-10-117-937-412 Sequence 412, App
759 20 27.8 9 4 US-10-215-272-39 Sequence 39, Appl
760 20 27.8 9 4 US-10-218-099-9 Sequence 9, Appl1
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762 20 27.8 9 4 US-10-685-977-67 Sequence 67, Appl
763 20 27.8 9 4 US-10-705-459-204 Sequence 204, App
764 20 27.8 9 5 US-10-715-976-39 Sequence 39, Appl1
765 20 27.8 9 5 US-10-862-195-1172 Sequence 1172, Ap
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771 20 27.8 9 6 US-11-012-787-187 Sequence 187, App
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773 20 27.8 9 6 US-11-067-155-412 Sequence 412, App
774 20 27.8 9 6 US-11-073-347-67 Sequence 67, Appl
775 20 27.8 9 6 US-11-045-024-132 Sequence 132, App
776 20 27.8 9 6 US-11-045-024-6319 Sequence 6319, Ap
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778 20 27.8 9 6 US-11-045-024-8933 Sequence 8933, Ap
779 20 27.8 9 6 US-11-045-024-11177 Sequence 11177, A
780 20 27.8 10 2 US-08-996-140-13 Sequence 13, Appl
781 20 27.8 10 3 US-09-056-160B-95 Sequence 95, Appl
782 20 27.8 10 3 US-09-834-765-97 Sequence 97, Appl1
783 20 27.8 10 3 US-09-834-765-333 Sequence 333, App
784 20 27.8 10 3 US-09-834-765-473 Sequence 473, App
785 20 27.8 10 3 US-09-891-823-73 Sequence 73, Appl
786 20 27.8 10 3 US-09-779-308-361 Sequence 361, App
787 20 27.8 10 3 US-09-935-430-417 Sequence 417, App
788 20 27.8 10 3 US-09-935-430-518 Sequence 518, App
789 20 27.8 10 3 US-09-572-404B-1350 Sequence 1350, Ap
790 20 27.8 10 3 US-09-572-404B-1934 Sequence 1934, Ap
791 20 27.8 10 3 US-09-572-404B-3710 Sequence 3710, Ap
792 20 27.8 10 3 US-09-572-404B-3116 Sequence 3116, Ap
793 20 27.8 10 3 US-09-820-053A-142 Sequence 142, App
794 20 27.8 10 3 US-09-573-822C-36 Sequence 36, Appl
795 20 27.8 10 3 US-09-573-822C-372 Sequence 372, Appl
796 20 27.8 10 3 US-09-573-822C-621 Sequence 621, App
797 20 27.8 10 3 US-09-573-822C-672 Sequence 672, App
798 20 27.8 10 3 US-09-899-575-130 Sequence 130, App
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ALIGNMENTS

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RESULT 1
US-10-884-862-219
; Sequence 219, Application US/10884862
; Publication No. US20050048071A1
GENERAL INFORMATION:
APPLICANT: BAE, Joo-eun
TITLE OF INVENTION: IMMUNOGENIC PEPTIDES
FILE REFERENCE: 047940-0239
CURRENT APPLICATION NUMBER: US/10/884, 862
CURRENT FILING DATE: 2004-07-02
PRIOR APPLICATION NUMBER: US 60/484689
PRIOR FILING DATE: 2003-07-03
NUMBER OF SEQ ID NOS: 328
SOFTWARE: PatentIn version 3.2
SEQ ID NO 219
; TYPE: PRT
; LENGTH: 9
; ORGANISM: Homo sapiens
US-10-884-862-219

Query Match 40.3%; Score 29; DB 5; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.9e+06;
Matches 5; Conservative 3; Mismatches 0; Gaps 0;
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QY 8 SVKSLYLG 15

Db 1 SIOSLFLG 8

RESULT 2
US-10-820-067A-361

; Sequence 361, Application US/10820067A
; Publication No. US20050214312A1

; GENERAL INFORMATION:

; APPLICANT: Fletcher, J.

; APPLICANT: Prince-Cohane, K.

; APPLICANT: Mehta, S.

; APPLICANT: Siusarewicz, P.

; APPLICANT: Andjelic, S.

; APPLICANT: Barber, B.

; TITLE OF INVENTION: IMPROVED HEAT SHOCK PROTEIN-BASED

; FILE REFERENCE: 8449-406-999

; CURRENT FILING DATE: 2004-04-08

; PRIOR FILING DATE: 2003-04-11

; PRIOR FILING DATE: 2003-04-18

; PRIOR FILING DATE: 2003-04-18

; PRIOR FILING DATE: 2003-09-16

; NUMBER OF SEQ ID NOS: 926

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 361

; LENGTH: 7

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Heat shock protein binding motif

US-10-820-067A-361

Query Match 38.9%; Score 28; DB 5; Length 7;

Best Local Similarity 71.4%; Pred. No. 1.9e+06;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 VKSLYLG 15

Db 1 VKKLYIG 7

RESULT 3

US-10-776-521B-152

; Sequence 152, Application US/10776521B

; Publication No. US20050202033A1

; GENERAL INFORMATION:

; APPLICANT: Fletcher, Jessica

; APPLICANT: Prince-Cohane, Kenya

; APPLICANT: Mehta, Sunil

; APPLICANT: Siusarewicz, Paul

; APPLICANT: Andjelic, Sofija

; APPLICANT: Barber, Brian

; TITLE OF INVENTION: IMPROVED HEAT SHOCK PROTEIN-BASED VACCINES AND

; FILE REFERENCE: 8449-405-999

; CURRENT FILING DATE: 2004-02-12

; PRIOR FILING DATE: 2003-09-16

; PRIOR FILING DATE: 2003-04-18

; PRIOR FILING DATE: 2003-04-18

; PRIOR FILING DATE: 2003-04-11

; PRIOR FILING DATE: 2003-02-13

; NUMBER OF SEQ ID NOS: 419

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 152

; LENGTH: 8

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Heat shock protein binding domain with a terminal

; OTHER INFORMATION: Tyr residue

US-10-776-521B-152

Query Match 38.9%; Score 28; DB 5; Length 8;

Best Local Similarity 71.4%; Pred. No. 1.9e+06;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 VKSLYLG 15

Db 1 VKKLYIG 7

RESULT 4

US-10-820-067A-648

; Sequence 648, Application US/10820067A

; Publication No. US20050214312A1

; GENERAL INFORMATION:

; APPLICANT: Fletcher, J.

; APPLICANT: Prince-Cohane, K.

; APPLICANT: Mehta, S.

; APPLICANT: Siusarewicz, P.

; APPLICANT: Andjelic, S.

; APPLICANT: Barber, B.

; TITLE OF INVENTION: IMPROVED HEAT SHOCK PROTEIN-BASED

; FILE REFERENCE: 8449-406-999

; CURRENT FILING DATE: 2004-04-08

; PRIOR FILING DATE: 2003-04-11

; PRIOR FILING DATE: 2003-04-18

; PRIOR FILING DATE: 2003-04-18

; PRIOR FILING DATE: 2003-09-16

; NUMBER OF SEQ ID NOS: 926

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 648

; LENGTH: 8

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Heat shock protein binding domain with a terminal

; OTHER INFORMATION: Tyr residue

US-10-820-067A-648

Query Match 38.9%; Score 28; DB 5; Length 8;

Best Local Similarity 71.4%; Pred. No. 1.9e+06;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 VKSLYLG 15

Db 1 VKKLYIG 7

RESULT 5

US-10-943-793-17

; Sequence 17, Application US/10943793

; Publication No. US20060063214A1

; GENERAL INFORMATION:

; APPLICANT: ALPER, OZGE

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING

; FILE REFERENCE: BIOS-003

; CURRENT FILING DATE: 2004-09-17

; PRIOR FILING DATE: 2004-09-17

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 17

; LENGTH: 15

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/ TYPE: PRT
/ ORGANISM: H. sapien
US-10-943-793-17

Query Match      37.5%; Score 27; DB 5; Length 15;
Best Local Similarity 85.7%; Pred. No. 8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 PFSVAKS 8
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Db      2 PFSVAVS 8

RESULT 6
US-09-852-910-81
; Sequence 81, Application US/09852910
; Publication No. US20030096297A1
; GENERAL INFORMATION:
; APPLICANT: Hamm, Heidi
; APPLICANT: Gilchrist, Annette
; TITLE OF INVENTION: Method For Identifying Inhibitors of G Protein Coupled Receptor S
; FILE REFERENCE: 2661-101
; CURRENT APPLICATION NUMBER: US/09/852,910
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US 60/275,472
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 271
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 81
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-852-910-81

Query Match      36.1%; Score 26; DB 3; Length 11;
Best Local Similarity 50.0%; Pred. No. 8.5e+02;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      5 VAKSVKSLYL 14
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Db      1 IAKNLKSMGL 10

RESULT 7
US-10-411-336A-81
; Sequence 81, Application US/10411336A
; Publication No. US20040018558A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrist, ANNETTE
; APPLICANT: HAMM, HEIDI
; TITLE OF INVENTION: METHOD FOR IDENTIFYING MODULATORS OF G PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: 2661-102
; CURRENT APPLICATION NUMBER: US/10/411,336A
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: US 09/852910
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/275472
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 81
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-411-336A-81

Query Match      36.1%; Score 26; DB 4; Length 11;
Best Local Similarity 50.0%; Pred. No. 8.5e+02;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      5 VAKSVKSLYL 14
       ||::||:|
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Db      1 IAKNLKSMGL 10

RESULT 8
US-09-563-222-35
; Sequence 35, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Hein, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; FILE REFERENCE: 310098.406
; CURRENT APPLICATION NUMBER: US/09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-563-222-35

Query Match      36.1%; Score 26; DB 3; Length 12;
Best Local Similarity 54.5%; Pred. No. 9.4e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      4 SVAKSVKSLYL 14
       |::|||
Db      1 SASSSVSSSYL 11

RESULT 9
US-10-461-878-1
; Sequence 1, Application US/10461878
; Publication No. US20040057902A1
; GENERAL INFORMATION:
; APPLICANT: GOLD, DAVID V.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: HANSEN, HANS J.
; TITLE OF INVENTION: MONOCLONAL ANTIBODY cPAM4
; FILE REFERENCE: 018733/1246
; CURRENT APPLICATION NUMBER: US/10/461,878
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/388,313
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: chimerized PAM4 antibody fragment
US-10-461-878-1

Query Match      36.1%; Score 26; DB 4; Length 12;
Best Local Similarity 54.5%; Pred. No. 9.4e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      4 SVAKSVKSLYL 14
       |::|||
Db      1 SASSSVSSSYL 11

RESULT 10
US-10-783-950-35
; Sequence 35, Application US/10783950
; Publication No. US20040199945A1
; GENERAL INFORMATION:
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.
; APPLICANT: HIATT, ANDREW C.
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; APPLICANT: HEIN, MICH B.
; FILE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 068904-0501
; CURRENT APPLICATION NUMBER: US/10/783,950
; PRIOR FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US/09/563,222
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-783-950-35
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Query Match          36.1%; Score 26; DB 4; Length 12;
Best Local Similarity 54.5%; Pred. No. 9.4e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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QY 4 SVAKSVKSLYL 14
   | : ||| |
Db 1 SASSSVSSSYL 11
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RESULT 11
US-10-461-885-1
; Sequence 1, Application US/10461885
; Publication No. US20050014207A1
; GENERAL INFORMATION:
; APPLICANT: GOLDBERG, DAVID M.
; APPLICANT: HANSEN, HANS J.
; APPLICANT: QU, ZHENGXING
; TITLE OF INVENTION: MONOCLONAL ANTIBODY hPAM4
; FILE REFERENCE: 018733-1215
; CURRENT APPLICATION NUMBER: US/10/461,885
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/388,314
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: humanized PAM4
; OTHER INFORMATION: antibody fragment
US-10-461-885-1
```

```
Query Match          36.1%; Score 26; DB 5; Length 12;
Best Local Similarity 54.5%; Pred. No. 9.4e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 4 SVAKSVKSLYL 14
   | : ||| |
Db 1 SASSSVSSSYL 11
```

```
RESULT 12
US-10-507-662-11
; Sequence 11, Application US/10507662
; Publication No. US20050255102A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; TITLE OF INVENTION: ANTI-ALPHA-V BETA-6 ANTIBODIES
; FILE REFERENCE: A136CCT
; CURRENT APPLICATION NUMBER: US/10/507,662
; CURRENT FILING DATE: 2004-09-13
```

```
; PRIOR APPLICATION NUMBER: 60/364,991
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/426,286
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-507-662-11
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```
Query Match          36.1%; Score 26; DB 5; Length 12;
Best Local Similarity 54.5%; Pred. No. 9.4e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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```
QY 4 SVAKSVKSLYL 14
   | : ||| |
Db 1 SASSSVSSSYL 11
```

```
RESULT 13
US-09-820-649-319
; Sequence 319, Application US/09820649
; Publication No. US2003019683A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 83 Human Secreted Proteins
; FILE REFERENCE: P2012P1
; CURRENT APPLICATION NUMBER: US/09/820,649
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US/09/236,557
; PRIOR FILING DATE: 1999-01-26
; PRIOR APPLICATION NUMBER: PCT/US98/15949
; PRIOR FILING DATE: 1998-07-29
; PRIOR APPLICATION NUMBER: 60/054,212
; PRIOR FILING DATE: 1997-07-30
; PRIOR APPLICATION NUMBER: 60/054,209
; PRIOR FILING DATE: 1997-07-30
; PRIOR APPLICATION NUMBER: 60/054,234
; PRIOR FILING DATE: 1997-07-30
; PRIOR APPLICATION NUMBER: 60/054,218
; PRIOR FILING DATE: 1997-07-30
; PRIOR APPLICATION NUMBER: 60/054,214
; PRIOR FILING DATE: 1997-07-30
; PRIOR APPLICATION NUMBER: 60/054,236
; PRIOR FILING DATE: 1997-07-30
; PRIOR APPLICATION NUMBER: 60/054,215
; PRIOR FILING DATE: 1997-07-30
; PRIOR APPLICATION NUMBER: 60/054,211
; PRIOR FILING DATE: 1997-07-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 353
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 319
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-820-649-319
```

```
Query Match          36.1%; Score 26; DB 3; Length 14;
Best Local Similarity 50.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 2 PFSVAKSV 9
   ||| : |
Db 3 PFSISYSI 10
```

```
RESULT 14
US-10-160-162-319
; Sequence 319, Application US/10160162
; Publication No. US20030166541A1
```

```
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: 83 Human Secreted Proteins
/ FILE REFERENCE: PZ012P2
/ CURRENT APPLICATION NUMBER: US/10/160,162
/ CURRENT FILING DATE: 2002-06-04
/ PRIOR APPLICATION NUMBER: 60/295,558
/ PRIOR FILING DATE: 2001-06-05
/ PRIOR APPLICATION NUMBER: 09/236,557
/ PRIOR FILING DATE: 1999-01-26
/ PRIOR APPLICATION NUMBER: PCT/US98/15949
/ PRIOR FILING DATE: 1998-07-29
/ PRIOR APPLICATION NUMBER: 60/054,212
/ PRIOR FILING DATE: 1997-07-30
/ PRIOR APPLICATION NUMBER: 60/054,209
/ PRIOR FILING DATE: 1997-07-30
/ PRIOR APPLICATION NUMBER: 60/054,234
/ PRIOR FILING DATE: 1997-07-30
/ PRIOR APPLICATION NUMBER: 60/054,218
/ PRIOR FILING DATE: 1997-07-30
/ PRIOR APPLICATION NUMBER: 60/054,214
/ PRIOR FILING DATE: 1997-07-30
/ PRIOR APPLICATION NUMBER: 60/054,236
/ PRIOR FILING DATE: 1997-07-30
/ PRIOR APPLICATION NUMBER: 60/054,215
/ PRIOR FILING DATE: 1997-07-30
/ PRIOR APPLICATION NUMBER: 60/054,211
/ PRIOR FILING DATE: 1997-07-30
/ PRIOR APPLICATION NUMBER: 60/054,217
/ PRIOR FILING DATE: 1997-07-30
/ PRIOR APPLICATION NUMBER: 60/054,213
/ PRIOR FILING DATE: 1997-07-30
/ PRIOR APPLICATION NUMBER: 60/055,968
/ PRIOR FILING DATE: 1997-08-18
/ PRIOR APPLICATION NUMBER: 60/055,969
/ PRIOR FILING DATE: 1997-08-18
/ PRIOR APPLICATION NUMBER: 60/055,972
/ PRIOR FILING DATE: 1997-08-18
/ PRIOR APPLICATION NUMBER: 60/056,561
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,534
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,729
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,543
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,727
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,554
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,730
/ PRIOR FILING DATE: 1997-08-19
/ NUMBER OF SEQ ID NOS: 353
/ SOFTWARE: Patentln Ver. 2.0
/ SEQ ID NO 319
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-160-162-319

Query Match      36.1%; Score 26; DB 4; Length 14;
Best Local Similarity 50.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      2 PPSVAKSV 9
      |||::|:
Db      3 PPSISYSI 10

RESULT 15
US-10-936-773-319
; Sequence 319, Application US/10936773
; Publication No. US20050037467A1

/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: 83 Human Secreted Proteins
/ FILE REFERENCE: PZ012P2
/ CURRENT APPLICATION NUMBER: US/10/936,773
/ CURRENT FILING DATE: 2004-09-09
/ PRIOR APPLICATION NUMBER: US/10/160,162
/ PRIOR FILING DATE: 2002-06-04
/ PRIOR APPLICATION NUMBER: 60/295,558
/ PRIOR FILING DATE: 2001-06-05
/ PRIOR APPLICATION NUMBER: 09/236,557
/ PRIOR FILING DATE: 1999-01-26
/ PRIOR APPLICATION NUMBER: PCT/US98/15949
/ PRIOR FILING DATE: 1998-07-29
/ PRIOR APPLICATION NUMBER: 60/054,212
/ PRIOR FILING DATE: 1997-07-30
/ PRIOR APPLICATION NUMBER: 60/054,209
/ PRIOR FILING DATE: 1997-07-30
/ PRIOR APPLICATION NUMBER: 60/054,234
/ PRIOR FILING DATE: 1997-07-30
/ PRIOR APPLICATION NUMBER: 60/054,218
/ PRIOR FILING DATE: 1997-07-30
/ PRIOR APPLICATION NUMBER: 60/054,214
/ PRIOR FILING DATE: 1997-07-30
/ PRIOR APPLICATION NUMBER: 60/054,236
/ PRIOR FILING DATE: 1997-07-30
/ PRIOR APPLICATION NUMBER: 60/054,215
/ PRIOR FILING DATE: 1997-07-30
/ PRIOR APPLICATION NUMBER: 60/054,211
/ PRIOR FILING DATE: 1997-07-30
/ PRIOR APPLICATION NUMBER: 60/054,217
/ PRIOR FILING DATE: 1997-07-30
/ PRIOR APPLICATION NUMBER: 60/054,213
/ PRIOR FILING DATE: 1997-07-30
/ PRIOR APPLICATION NUMBER: 60/055,968
/ PRIOR FILING DATE: 1997-08-18
/ PRIOR APPLICATION NUMBER: 60/055,969
/ PRIOR FILING DATE: 1997-08-18
/ PRIOR APPLICATION NUMBER: 60/055,972
/ PRIOR FILING DATE: 1997-08-18
/ PRIOR APPLICATION NUMBER: 60/056,561
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,534
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,729
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,543
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,727
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,554
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,730
/ PRIOR FILING DATE: 1997-08-19
/ NUMBER OF SEQ ID NOS: 596
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 500
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-907-969-500

Query Match      36.1%; Score 26; DB 5; Length 14;
Best Local Similarity 50.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      2 PPSVAKSV 9
      |||::|:
Db      3 PPSISYSI 10

RESULT 16
US-09-907-969-500
; Sequence 500, Application US/09907969
; Publication No. US20030091580A1
/ GENERAL INFORMATION:
/ APPLICANT: Mitcham, Jennifer L.
/ APPLICANT: King, Gordon E.
/ APPLICANT: Algate, Paul A.
/ APPLICANT: Fling, Steven P.
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Fanger, Gary Richard
/ APPLICANT: Reed, Steven G.
/ APPLICANT: Vedvick, Thomas S.
/ APPLICANT: Carter, Darrick
/ APPLICANT: Hill, Paul
/ APPLICANT: Albone, Bart
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
/ TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
/ FILE REFERENCE: 210121.462C8
/ CURRENT APPLICATION NUMBER: US/09/907,969
/ CURRENT FILING DATE: 2001-07-17
/ NUMBER OF SEQ ID NOS: 596
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 500
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-907-969-500
```

Query Match 36.1%; Score 26; DB 3; Length 15;
Best Local Similarity 53.8%; Pred. No. 1.2e+03;
Matches 7; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY 2 PFSVAKSVKSLYL 14
DB 2 PYSLDKD--SLYL 12

RESULT 17

US-10-198-053-500
; Sequence 500, Application US/10198053
; Publication No. US20030124140A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hill, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C9
; CURRENT APPLICATION NUMBER: US/10/198.053
; CURRENT FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 500
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-198-053-500

Query Match 36.1%; Score 26; DB 4; Length 15;
Best Local Similarity 53.8%; Pred. No. 1.2e+03;
Matches 7; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY 2 PFSVAKSVKSLYL 14
DB 2 PYSLDKD--SLYL 12

RESULT 18
US-10-431-096-289
; Sequence 289, Application US/10431096
; Publication No. US20040086896A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB
; FILE REFERENCE: D0108A CIP
; CURRENT APPLICATION NUMBER: US/10/431.096
; CURRENT FILING DATE: 2003-05-07
; PRIOR APPLICATION NUMBER: US 60/284,962
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 10/126,103
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/286,645
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: US 60/346,986
; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 289
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-431-096-289

Query Match 36.1%; Score 26; DB 4; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 VPFSVAKSVK 10
DB 1 VPFSVAKSVK 10

DB 2 VPISDSKSIQ 11

RESULT 19
US-10-860-790-500
; Sequence 500, Application US/10860790
; Publication No. US20050031634A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hill, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C11
; CURRENT APPLICATION NUMBER: US/10/860.790
; CURRENT FILING DATE: 2004-06-02
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 500
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-860-790-500

Query Match 36.1%; Score 26; DB 5; Length 15;
Best Local Similarity 53.8%; Pred. No. 1.2e+03;
Matches 7; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY 2 PFSVAKSVKSLYL 14
DB 2 PYSLDKD--SLYL 12

RESULT 20
US-10-676-909-53
; Sequence 53, Application US/10676909
; Publication No. US20040086521A1
; GENERAL INFORMATION:
; APPLICANT: KROPSHOFER, H.
; APPLICANT: VOGT, A.
; TITLE OF INVENTION: Method for the identification of antigenic peptides associated t
; FILE REFERENCE: 21388
; CURRENT APPLICATION NUMBER: US/10/676.909
; CURRENT FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: EP 02022223.8
; PRIOR FILING DATE: 2002-02-10
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 53
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-676-909-53

Query Match 35.4%; Score 25.5; DB 4; Length 14;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 6; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

QY 4 SVAKSVKSL-YL 14
DB 2 AVYKSIKSIPIYL 13

RESULT 21
US-10-676-909-54
; Sequence 54, Application US/10676909
; Publication No. US20040086521A1
; GENERAL INFORMATION:
; APPLICANT: KROPSHOFER, H.
; APPLICANT: VOGT, A.
; TITLE OF INVENTION: Method for the identification of antigenic peptides associated t

```

; TITLE OF INVENTION: diseases
; FILE REFERENCE: 21388
; CURRENT APPLICATION NUMBER: US/10/676,909
; CURRENT FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: EP 02022223.8
; PRIOR FILING DATE: 2002-02-10
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 54
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-676-909-54

Query Match          35.4%; Score 25; DB 4; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.5e+03;
Matches 6; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

QY      4 SVAKSVKSL-YL 14
       : |||:|:|
Db      3 AVVKSRISIPYL 14

RESULT 22
US-09-920-480B-9
; Sequence 9, Application US/09920480B
; Publication No. US20040014697A1
; GENERAL INFORMATION:
; APPLICANT: Nicolette, Charles A.
; TITLE OF INVENTION: MELANOMA ANTIGENIC PEPTIDES
; FILE REFERENCE: GZ 2063.10
; CURRENT APPLICATION NUMBER: US/09/920,480B
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 09/249,272
; PRIOR FILING DATE: 1999-02-11
; PRIOR APPLICATION NUMBER: 60/103,229
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-920-480B-9

Query Match          34.7%; Score 25; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VPFVS 5
       : |||
Db      4 VPFVS 8

RESULT 23
US-10-333-430-17
; Sequence 17, Application US/10333430
; Publication No. US20040072240A1
; GENERAL INFORMATION:
; APPLICANT: INSTITUTE GUSTAVE ROUSSY
; APPLICANT: KOSMATOPOULOS, Kostas
; APPLICANT: TOURDOT, Sophie
; APPLICANT: SCARDINO, Antonio
; TITLE OF INVENTION: METHOD FOR SCREENING PEPTIDES FOR USE IN
; TITLE OF INVENTION: IMMUNOTHERAPY
; FILE REFERENCE: 33339/259034
; CURRENT APPLICATION NUMBER: US/10/333,430
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: FR 0009591
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 70
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```

; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 17
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-333-430-17

Query Match          34.7%; Score 25; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VPFVS 5
       : |||
Db      4 VPFVS 8

RESULT 24
US-09-847-185-30
; Sequence 30, Application US/09847185
; Patent No. US20020076392A1
; GENERAL INFORMATION:
; APPLICANT: SOO HOO, William
; TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS
; COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE
; RESPONSE USING SAME
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSER: CAMPBELL & FLORES, LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/847,185
; FILING DATE: 01-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/201,931
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-1M 2442
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)535-9001
; TELEFAX: (619)535-8949
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-847-185-30

Query Match          34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VPFVS 5
       : |||
Db      5 VPFVS 9

RESULT 25
```

US-09-862-260A-3
; Sequence 3, Application US/09862260A
; Patent No. US20020082217A1
; GENERAL INFORMATION:
; APPLICANT: Nicolette, Charles A.
; TITLE OF INVENTION: THERAPEUTIC ANTI-MELANOMA COMPOUNDS
; FILE REFERENCE: 126881210200
; CURRENT APPLICATION NUMBER: US/09/862,260A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/208,955
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 60/267,877
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-862-260A-3

Query Match 34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPSV 5
| | | | |
Db 5 VPSV 9

RESULT 26
US-09-862-260A-23
; Sequence 23, Application US/09862260A
; Patent No. US20020082217A1
; GENERAL INFORMATION:
; APPLICANT: Nicolette, Charles A.
; TITLE OF INVENTION: THERAPEUTIC ANTI-MELANOMA COMPOUNDS
; FILE REFERENCE: 126881210200
; CURRENT APPLICATION NUMBER: US/09/862,260A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/208,955
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 60/267,877
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-862-260A-23

Query Match 34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPSV 5
| | | | |
Db 5 VPSV 9

RESULT 27
US-09-923-831-31
; Sequence 31, Application US/09923831
; Patent No. US20020115142A1
; GENERAL INFORMATION:
; APPLICANT: Martelange, Val,rie
; APPLICANT: De Smet, Charles
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR
; FILE REFERENCE: L0461/7054
; CURRENT APPLICATION NUMBER: US/09/923,831
; CURRENT FILING DATE: 2001-08-07

; PRIOR APPLICATION NUMBER: 09/183,706
; PRIOR FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 43
; SEQ ID NO 31
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-923-831-31

Query Match 34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPSV 5
| | | | |
Db 5 VPSV 9

RESULT 28
US-09-872-832-45
; Sequence 45, Application US/09872832
; Patent No. US20020131960A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center
; TITLE OF INVENTION: ARTIFICIAL ANTIGEN PRESENTING CELLS AND METHODS OF USE THEREOF
; FILE REFERENCE: 830002-2003.1
; CURRENT APPLICATION NUMBER: US/09/872,832
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/209,157
; PRIOR FILING DATE: 2000-02-06
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(9)
; OTHER INFORMATION: gp-100 modified peptide
US-09-872-832-45

Query Match 34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPSV 5
| | | | |
Db 5 VPSV 9

RESULT 29
US-09-766-889A-43
; Sequence 43, Application US/09766889A
; Patent No. US20020164654A1
; GENERAL INFORMATION:
; APPLICANT: Luiten, Rosalie
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Stroobant, Vincent
; APPLICANT: Demotte, Nathalie
; APPLICANT: Schultz, Erwin
; TITLE OF INVENTION: MAGE ANTIGENIC PEPTIDES WHICH BIND HLA-B35 AND HLA-B44
; FILE REFERENCE: L0461/7104
; CURRENT APPLICATION NUMBER: US/09/766,889A
; CURRENT FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/177,242
; PRIOR FILING DATE: 2000-01-20
; PRIOR APPLICATION NUMBER: US 60/243,212
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43

```
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-766-889A-43
```

```
Query Match          34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VPFVS 5
    |||||
Db 5 VPFVS 9
```

```
RESULT 30
US-09-812-238B-3
; Sequence 3, Application US/09812238B
; Patent No. US20020169132A1
; GENERAL INFORMATION:
; APPLICANT: Nicolette, Charles
; TITLE OF INVENTION: THERAPEUTIC ANTI-MELANOMA COMPOUNDS
; FILE REFERENCE: GZ 2094.00
; CURRENT APPLICATION NUMBER: US/09/812,238B
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-812-238B-3
```

```
Query Match          34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VPFVS 5
    |||||
Db 5 VPFVS 9
```

```
RESULT 31
US-09-812-238B-5
; Sequence 5, Application US/09812238B
; Patent No. US20020169132A1
; GENERAL INFORMATION:
; APPLICANT: Nicolette, Charles
; TITLE OF INVENTION: THERAPEUTIC ANTI-MELANOMA COMPOUNDS
; FILE REFERENCE: GZ 2094.00
; CURRENT APPLICATION NUMBER: US/09/812,238B
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-812-238B-5
```

```
Query Match          34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VPFVS 5
    |||||
Db 5 VPFVS 9
```

```
RESULT 32
US-09-812-238B-7
; Sequence 7, Application US/09812238B
; Patent No. US20020169132A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Nicolette, Charles
; TITLE OF INVENTION: THERAPEUTIC ANTI-MELANOMA COMPOUNDS
; FILE REFERENCE: GZ 2094.00
; CURRENT APPLICATION NUMBER: US/09/812,238B
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-812-238B-7
```

```
Query Match          34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VPFVS 5
    |||||
Db 5 VPFVS 9
```

```
RESULT 33
US-09-812-238B-9
; Sequence 9, Application US/09812238B
; Patent No. US20020169132A1
; GENERAL INFORMATION:
; APPLICANT: Nicolette, Charles
; TITLE OF INVENTION: THERAPEUTIC ANTI-MELANOMA COMPOUNDS
; FILE REFERENCE: GZ 2094.00
; CURRENT APPLICATION NUMBER: US/09/812,238B
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-812-238B-9
```

```
Query Match          34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VPFVS 5
    |||||
Db 5 VPFVS 9
```

```
RESULT 34
US-09-812-238B-11
; Sequence 11, Application US/09812238B
; Patent No. US20020169132A1
; GENERAL INFORMATION:
; APPLICANT: Nicolette, Charles
; TITLE OF INVENTION: THERAPEUTIC ANTI-MELANOMA COMPOUNDS
; FILE REFERENCE: GZ 2094.00
; CURRENT APPLICATION NUMBER: US/09/812,238B
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-812-238B-11
```

```
Query Match          34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VPFVS 5
    |||||
```

Db 5 VPFSV 9

RESULT 35
US-09-812-238B-13
; Sequence 13, Application US/09812238B
; Patent No. US20020169132A1
; GENERAL INFORMATION:
; APPLICANT: Nicolette, Charles
; TITLE OF INVENTION: THERAPEUTIC ANTI-MELANOMA COMPOUNDS
; FILE REFERENCE: GZ 2094.00
; CURRENT APPLICATION NUMBER: US/09/812,238B
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-812-238B-13

Query Match 34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFSV 5
|||||
Db 5 VPFSV 9

RESULT 36
US-09-812-238B-15
; Sequence 15, Application US/09812238B
; Patent No. US20020169132A1
; GENERAL INFORMATION:
; APPLICANT: Nicolette, Charles
; TITLE OF INVENTION: THERAPEUTIC ANTI-MELANOMA COMPOUNDS
; FILE REFERENCE: GZ 2094.00
; CURRENT APPLICATION NUMBER: US/09/812,238B
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-812-238B-15

Query Match 34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFSV 5
|||||
Db 5 VPFSV 9

RESULT 37
US-09-812-238B-17
; Sequence 17, Application US/09812238B
; Patent No. US20020169132A1
; GENERAL INFORMATION:
; APPLICANT: Nicolette, Charles
; TITLE OF INVENTION: THERAPEUTIC ANTI-MELANOMA COMPOUNDS
; FILE REFERENCE: GZ 2094.00
; CURRENT APPLICATION NUMBER: US/09/812,238B
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-812-238B-17

Query Match 34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFSV 5
|||||
Db 5 VPFSV 9

RESULT 38
US-09-812-238B-19
; Sequence 19, Application US/09812238B
; Patent No. US20020169132A1
; GENERAL INFORMATION:
; APPLICANT: Nicolette, Charles
; TITLE OF INVENTION: THERAPEUTIC ANTI-MELANOMA COMPOUNDS
; FILE REFERENCE: GZ 2094.00
; CURRENT APPLICATION NUMBER: US/09/812,238B
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-812-238B-19

Query Match 34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFSV 5
|||||
Db 5 VPFSV 9

RESULT 39
US-09-909-460-62
; Sequence 62, Application US/09909460
; Publication No. US20020182258A1
; GENERAL INFORMATION:
; APPLICANT: Lunsford, Lynn B.
; APPLICANT: Putnam, David
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY OF NUCLEIC
; FILE REFERENCE: 08191/014001
; CURRENT APPLICATION NUMBER: US/09/909,460
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/321,346
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-27
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 62
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-909-460-62

Query Match 34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFSV 5
|||||
Db 5 VPFSV 9

RESULT 40
US-09-865-548A-42
; Sequence 42, Application US/09865548A

Publication No. US20030096298A1
GENERAL INFORMATION:
APPLICANT: Barnea, Eilon
APPLICANT: Beer, Ilan
APPLICANT: Ziv, Tamir
APPLICANT: Admon, Arie
TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES CAPABLE OF BINDING TO MHC MOLECULE
FILE REFERENCE: 01/22080
CURRENT APPLICATION NUMBER: US/09/865,548A
CURRENT FILING DATE: 2001-05-16
PRIOR FILING DATE: 2001-05-16
NUMBER OF SEQ ID NOS: 204
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 42
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic peptide
US-09-865-548A-42

Query Match 34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VFPSV 5
Db 5 VFPSV 9

RESULT 41
US-09-898-860-48
Sequence 48, Application US/09898860
Publication No. US20030144482A1
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG, STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND THEIR USE IN DIAGNOSTIC AND THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792

INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-09-898-860-48

Query Match 34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VFPSV 5
Db 5 VFPSV 9

RESULT 42
US-09-898-860-83
Sequence 83, Application US/09898860
Publication No. US20030144482A1
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG, STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND THEIR USE IN DIAGNOSTIC AND THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 83:
US-09-898-860-83

Query Match 34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFVS 5
|||
Db 5 VPFVS 9

RESULT 43

US-09-898-860-84
; Sequence 84, Application US/09898860
; Publication No. US20030144482A1

GENERAL INFORMATION:

APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
STEVEN A.

TITLE OF INVENTION: MELANOMA ANTIGENS AND
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS

NUMBER OF SEQUENCES: 126

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/898,860

FILING DATE: 03-Jul-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/267,439

FILING DATE: <Unknown>

APPLICATION NUMBER: US/08/417,174

FILING DATE: 05-APR-1995

APPLICATION NUMBER: US/08/231,565

FILING DATE: 22-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: CAROL M. GRUPPI

REGISTRATION NUMBER: 37,341

REFERENCE/DOCKET NUMBER: 2026-4124US1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 758-4800

TELEX: 421792

INFORMATION FOR SEQ ID NO: 84:

SEQUENCE CHARACTERISTICS:

LENGTH: 9

TYPE: amino acid

STRANDEDNESS: Unknown

TOPOLOGY: Unknown

MOLECULE TYPE: Peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 84:

US-09-898-860-84

Query Match 34.7%; Score 25; DB 3; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.9e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFVS 5
|||
Db 5 VPFVS 9

RESULT 44

US-09-898-860-85

; Sequence 85, Application US/09898860

; Publication No. US20030144482A1

GENERAL INFORMATION:

APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
STEVEN A.

TITLE OF INVENTION: MELANOMA ANTIGENS AND
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS

NUMBER OF SEQUENCES: 126

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/898,860

FILING DATE: 03-Jul-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/267,439

FILING DATE: <Unknown>

APPLICATION NUMBER: US/08/417,174

FILING DATE: 05-APR-1995

APPLICATION NUMBER: US/08/231,565

FILING DATE: 22-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: CAROL M. GRUPPI

REGISTRATION NUMBER: 37,341

REFERENCE/DOCKET NUMBER: 2026-4124US1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 758-4800

TELEX: 421792

INFORMATION FOR SEQ ID NO: 85:

SEQUENCE CHARACTERISTICS:

LENGTH: 9

TYPE: amino acid

STRANDEDNESS: Unknown

TOPOLOGY: Unknown

MOLECULE TYPE: Peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 85:

US-09-898-860-85

Query Match 34.7%; Score 25; DB 3; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.9e+06; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFVS 5
|||
Db 5 VPFVS 9

RESULT 45

US-09-898-860-86

; Sequence 86, Application US/09898860

; Publication No. US20030144482A1

GENERAL INFORMATION:

APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
STEVEN A.

TITLE OF INVENTION: MELANOMA ANTIGENS AND
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS

NUMBER OF SEQUENCES: 126

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/898,860
FILING DATE: 03-Jul-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE: <Unknown>
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 86:
US-09-898-860-86

Query Match 34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPPSV 5
Db 5 VPPSV 9

RESULT 46
US-09-898-860-87
Sequence 87, Application US/09898860
Publication No. US20030144482A1
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/898,860
FILING DATE: 03-Jul-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE: <Unknown>
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994

ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 87:
US-09-898-860-87

Query Match 34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPPSV 5
Db 5 VPPSV 9

RESULT 47
US-09-898-860-88
Sequence 88, Application US/09898860
Publication No. US20030144482A1
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/898,860
FILING DATE: 03-Jul-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE: <Unknown>
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown

TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 88:
US-09-898-860-88

Query Match 34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPPSV 5
| | | | |
DB 5 VPPSV 9

RESULT 48
US-09-898-860-89
Sequence 89, Application US/09898860
Publication No. US20030144482A1
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/898,860
FILING DATE: 03-Jul-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE: <Unknown>
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 89:
US-09-898-860-89

Query Match 34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPPSV 5
| | | | |
DB 5 VPPSV 9

RESULT 49
US-09-898-860-90
Sequence 90, Application US/09898860
Publication No. US20030144482A1
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
STEVEN A.

TITLE OF INVENTION: MELANOMA ANTIGENS AND
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS

NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/898,860
FILING DATE: 03-Jul-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE: <Unknown>

APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792

INFORMATION FOR SEQ ID NO: 90:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 90:
US-09-898-860-90

Query Match 34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPPSV 5
| | | | |
DB 5 VPPSV 9

RESULT 50
US-09-898-860-91

Sequence 91, Application US/09898860
Publication No. US20030144482A1
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
STEVEN A.

TITLE OF INVENTION: MELANOMA ANTIGENS AND
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS

NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:

```

; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/898,860
; FILING DATE: 03-Jul-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/267,439
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/08/417,174
; FILING DATE: 05-APR-1995
; APPLICATION NUMBER: US/08/231,565
; FILING DATE: 22-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: CAROL M. GRUPPI
; REGISTRATION NUMBER: 37,341
; REFERENCE/DOCKET NUMBER: 2026-4124US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 91:
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9
; TYPE: amino acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 91:
US-09-898-860-91

Query Match          34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPPSV 5
Db 5 VPPSV 9

RESULT 51
US-09-898-860-92
; Sequence 92, Application US/09898860
; Publication No. US20030144482A1
; GENERAL INFORMATION:
; APPLICANT: KAWAKAMI, YUTAKA, ROSENBERG,
; STEVEN A.
; TITLE OF INVENTION: MELANOMA ANTIGENS AND
; THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
; METHODS
; NUMBER OF SEQUENCES: 126
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/898,860
```

```

; FILING DATE: 03-Jul-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/267,439
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/08/417,174
; FILING DATE: 05-APR-1995
; APPLICATION NUMBER: US/08/231,565
; FILING DATE: 22-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: CAROL M. GRUPPI
; REGISTRATION NUMBER: 37,341
; REFERENCE/DOCKET NUMBER: 2026-4124US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 92:
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9
; TYPE: amino acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 92:
US-09-898-860-92

Query Match          34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPPSV 5
Db 5 VPPSV 9

RESULT 52
US-09-898-860-93
; Sequence 93, Application US/09898860
; Publication No. US20030144482A1
; GENERAL INFORMATION:
; APPLICANT: KAWAKAMI, YUTAKA, ROSENBERG,
; STEVEN A.
; TITLE OF INVENTION: MELANOMA ANTIGENS AND
; THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
; METHODS
; NUMBER OF SEQUENCES: 126
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/898,860
; FILING DATE: 03-Jul-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/267,439
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/08/417,174
; FILING DATE: 05-APR-1995
; APPLICATION NUMBER: US/08/231,565
; FILING DATE: 22-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: CAROL M. GRUPPI
; REGISTRATION NUMBER: 37,341
; REFERENCE/DOCKET NUMBER: 2026-4124US1
; TELECOMMUNICATION INFORMATION:
```

TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELE: 421792
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 93:
US-09-898-860-93

Query Match 34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPPSV 5
Db 5 VPPSV 9

RESULT 53
US-09-898-860-94
Sequence 94, Application US/09898860
Publication No. US20030144482A1
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/898,860
FILING DATE: 03-Jul-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE: <Unknown>
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 94:
US-09-898-860-94

Query Match 34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPPSV 5
Db 5 VPPSV 9

RESULT 54
US-09-898-860-95
Sequence 95, Application US/09898860
Publication No. US20030144482A1
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/898,860
FILING DATE: 03-Jul-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE: <Unknown>
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 95:
US-09-898-860-95

Query Match 34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPPSV 5
Db 5 VPPSV 9

RESULT 55
US-09-898-860-96
Sequence 96, Application US/09898860
Publication No. US20030144482A1

GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/898,860
FILING DATE: 03-Jul-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE: <Unknown>
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 96:
US-09-898-860-96
Query Match 34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPFSV 5
|||
5 VPFSV 9
Db
RESULT 56
US-09-898-860-97
Sequence 97, Application US/09898860
Publication No. US20030144482A1
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA

ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/898,860
FILING DATE: 03-Jul-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE: <Unknown>
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 97:
US-09-898-860-97
Query Match 34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPFSV 5
|||
5 VPFSV 9
Db
RESULT 57
US-09-898-860-98
Sequence 98, Application US/09898860
Publication No. US20030144482A1
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/898,860
FILING DATE: 03-Jul-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE: <Unknown>
APPLICATION NUMBER: US/08/417,174

FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 98:
US-09-898-860-98

Query Match 34.7% Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFSV 5
Db 5 VPFSV 9

RESULT 58

US-09-898-860-99
Sequence 99, Application US/09898860
Publication No. US20030144482A1

GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA, ROSENBERG,
STEVEN A.

TITLE OF INVENTION: MELANOMA ANTIGENS AND
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS

NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/898,860

FILING DATE: 03-Jul-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/267,439

FILING DATE: <Unknown>

APPLICATION NUMBER: US/08/417,174

FILING DATE: 05-APR-1995

APPLICATION NUMBER: US/08/231,565

FILING DATE: 22-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: CAROL M. GRUPPI

REGISTRATION NUMBER: 37,341

REFERENCE/DOCKET NUMBER: 2026-4124US1

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:

LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 99:
US-09-898-860-99

Query Match 34.7% Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFSV 5
Db 5 VPFSV 9

RESULT 59

US-09-898-860-100
Sequence 100, Application US/09898860
Publication No. US20030144482A1

GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA, ROSENBERG,
STEVEN A.

TITLE OF INVENTION: MELANOMA ANTIGENS AND
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS

NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/898,860

FILING DATE: 03-Jul-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/267,439

FILING DATE: <Unknown>

APPLICATION NUMBER: US/08/417,174

FILING DATE: 05-APR-1995

APPLICATION NUMBER: US/08/231,565

FILING DATE: 22-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: CAROL M. GRUPPI

REGISTRATION NUMBER: 37,341

REFERENCE/DOCKET NUMBER: 2026-4124US1

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:

LENGTH: 9
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-09-898-860-100

Query Match 34.7% Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFSV 5

Db 5 VPF5V 9

|||||

RESULT 60

US-09-898-860-101

Sequence 101, Application US/09898860

Publication No. US20030144482A1

GENERAL INFORMATION:

APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG, STEVEN A.

TITLE OF INVENTION: MELANOMA ANTIGENS AND THEIR USE IN DIAGNOSTIC AND THERAPEUTIC METHODS

NUMBER OF SEQUENCES: 126

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/898,860

FILING DATE: 03-Jul-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/267,439

FILING DATE: <Unknown>

APPLICATION NUMBER: US/08/417,174

FILING DATE: 05-APR-1995

APPLICATION NUMBER: US/08/231,565

FILING DATE: 22-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: CAROL M. GRUPPI

REGISTRATION NUMBER: 37,341

REFERENCE/DOCKET NUMBER: 2026-4124US1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 758-4800

TELEFAX: (212) 751-6849

INFORMATION FOR SEQ ID NO: 101:

SEQUENCE CHARACTERISTICS:

LENGTH: 9

TYPE: amino acid

STRANDEDNESS: Unknown

TOPOLOGY: Unknown

MOLECULE TYPE: Peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 101:

US-09-898-860-101

Query Match 34.7%; Score 25; DB 3; Length 9;

Best Local Similarity 100.0%; Pred.No. 1.9e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPF5V 5

|||||

Db 5 VPF5V 9

RESULT 61

US-09-898-860-102

Sequence 102, Application US/09898860

Publication No. US20030144482A1

GENERAL INFORMATION:

APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG, STEVEN A.

TITLE OF INVENTION: MELANOMA ANTIGENS AND THEIR USE IN DIAGNOSTIC AND THERAPEUTIC METHODS

NUMBER OF SEQUENCES: 126

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

|||||

METHODS

NUMBER OF SEQUENCES: 126

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/898,860

FILING DATE: 03-Jul-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/267,439

FILING DATE: <Unknown>

APPLICATION NUMBER: US/08/417,174

FILING DATE: 05-APR-1995

APPLICATION NUMBER: US/08/231,565

FILING DATE: 22-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: CAROL M. GRUPPI

REGISTRATION NUMBER: 37,341

REFERENCE/DOCKET NUMBER: 2026-4124US1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 758-4800

TELEFAX: (212) 751-6849

INFORMATION FOR SEQ ID NO: 102:

SEQUENCE CHARACTERISTICS:

LENGTH: 9

TYPE: amino acid

STRANDEDNESS: Unknown

TOPOLOGY: Unknown

MOLECULE TYPE: Peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 102:

US-09-898-860-102

Query Match 34.7%; Score 25; DB 3; Length 9;

Best Local Similarity 100.0%; Pred.No. 1.9e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPF5V 5

|||||

Db 5 VPF5V 9

RESULT 62

US-09-898-860-103

Sequence 103, Application US/09898860

Publication No. US20030144482A1

GENERAL INFORMATION:

APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG, STEVEN A.

TITLE OF INVENTION: MELANOMA ANTIGENS AND THEIR USE IN DIAGNOSTIC AND THERAPEUTIC METHODS

NUMBER OF SEQUENCES: 126

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS


```
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/698,860
  FILING DATE: 03-Jul-2001
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US/09/267,439
  FILING DATE: <Unknown>
  APPLICATION NUMBER: US/08/417,174
  FILING DATE: 05-APR-1995
  APPLICATION NUMBER: US/08/231,565
  FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
  NAME: CAROL M. GRUPPI
  REGISTRATION NUMBER: 37,341
  REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (212) 758-4800
  TELEFAX: (212) 751-6849
  TELEX: 421792
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
  LENGTH: 9
  TYPE: amino acid
  STRANDEDNESS: Unknown
  TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 103:
US-09-898-860-103
```

```
Query Match          34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VPSV 5
        |||||
Db      5 VPSV 9
```

```
RESULT 63
US-09-920-480B-5
; Sequence 5, Application US/09920480B
; Publication No. US20040014697A1
; GENERAL INFORMATION:
; APPLICANT: Nicolette, Charles A.
; TITLE OF INVENTION: MELANOMA ANTIGENIC PEPTIDES
; FILE REFERENCE: GZ 2063.10
; CURRENT APPLICATION NUMBER: US/09/920,480B
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 09/249,272
; PRIOR FILING DATE: 1999-02-11
; PRIOR APPLICATION NUMBER: 60/103,229
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-920-480B-5
```

```
Query Match          34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VPSV 5
        |||||
Db      5 VPSV 9
```

```
RESULT 64
US-09-920-480B-6
; Sequence 6, Application US/09920480B
; Publication No. US20040014697A1
```

```
GENERAL INFORMATION:
  APPLICANT: Nicolette, Charles A.
  TITLE OF INVENTION: MELANOMA ANTIGENIC PEPTIDES
  FILE REFERENCE: GZ 2063.10
CURRENT APPLICATION NUMBER: US/09/920,480B
CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 09/249,272
PRIOR FILING DATE: 1999-02-11
PRIOR APPLICATION NUMBER: 60/103,229
PRIOR FILING DATE: 1998-10-05
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-920-480B-6
```

```
Query Match          34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VPSV 5
        |||||
Db      5 VPSV 9
```

```
RESULT 65
US-09-920-480B-7
; Sequence 7, Application US/09920480B
; Publication No. US20040014697A1
; GENERAL INFORMATION:
; APPLICANT: Nicolette, Charles A.
; TITLE OF INVENTION: MELANOMA ANTIGENIC PEPTIDES
; FILE REFERENCE: GZ 2063.10
; CURRENT APPLICATION NUMBER: US/09/920,480B
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 09/249,272
; PRIOR FILING DATE: 1999-02-11
; PRIOR APPLICATION NUMBER: 60/103,229
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-920-480B-7
```

```
Query Match          34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VPSV 5
        |||||
Db      5 VPSV 9
```

```
RESULT 66
US-09-920-480B-8
; Sequence 8, Application US/09920480B
; Publication No. US20040014697A1
; GENERAL INFORMATION:
; APPLICANT: Nicolette, Charles A.
; TITLE OF INVENTION: MELANOMA ANTIGENIC PEPTIDES
; FILE REFERENCE: GZ 2063.10
; CURRENT APPLICATION NUMBER: US/09/920,480B
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 09/249,272
; PRIOR FILING DATE: 1999-02-11
; PRIOR APPLICATION NUMBER: 60/103,229
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 9
```

```
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 8
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
US-09-920-480B-8
```

```
Query Match          34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VPFVS 5
        |||||
Db       5 VPFVS 9
```

```
RESULT 67
US-09-872-836-62
 ; Sequence 62, Application US/09872836
 ; Publication No. US20040142475A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Barman, Shikha P.
 ; APPLICANT: McKeever, Una
 ; APPLICANT: Hedley, Mary Lynne
 ; TITLE OF INVENTION: DELIVERY SYSTEMS FOR BIOACTIVE AGENTS
 ; FILE REFERENCE: 08191-018001
 ; CURRENT APPLICATION NUMBER: US/09/872,836
 ; CURRENT FILING DATE: 2001-06-01
 ; PRIOR APPLICATION NUMBER: US 60/208,830
 ; PRIOR FILING DATE: 2000-06-02
 ; NUMBER OF SEQ ID NOS: 120
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 62
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
US-09-872-836-62
```

```
Query Match          34.7%; Score 25; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VPFVS 5
        |||||
Db       5 VPFVS 9
```

```
RESULT 68
US-10-106-487-3
 ; Sequence 3, Application US/10106487
 ; Publication No. US20020164721A1
 ; GENERAL INFORMATION:
 ; APPLICANT: FIRAT, HUSEYIN
 ; APPLICANT: LEMONNIER, FRANCOIS
 ; APPLICANT: LANGLADE-DEMOYEN, PIERRE
 ; APPLICANT: MICHEL, MARIE-LOUISE
 ; TITLE OF INVENTION: DESIGN OF A POLYPEPTIDIC CONSTRUCT FOR THE INDUCTION
 ; TITLE OF INVENTION: OF
 ; TITLE OF INVENTION: HLA-A2.1 RESTRICTED HIV 1 SPECIFIC CTL RESPONSES USING
 ; FILE REFERENCE: 03495.0196 SEQUENCE LISTING
 ; CURRENT APPLICATION NUMBER: US/10/106,487
 ; CURRENT FILING DATE: 2002-03-27
 ; PRIOR APPLICATION NUMBER: 09/675,673
 ; PRIOR FILING DATE: 2000-09-29
 ; PRIOR APPLICATION NUMBER: 60/158,356
 ; PRIOR FILING DATE: 1999-10-12
 ; NUMBER OF SEQ ID NOS: 41
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
```

```
US-10-106-487-3
```

```
Query Match          34.7%; Score 25; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VPFVS 5
        |||||
Db       5 VPFVS 9
```

```
RESULT 69
US-10-047-539-6
 ; Sequence 6, Application US/10047539
 ; Publication No. US20020177547A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KOLLING, KARIN
 ; APPLICANT: PAVLOVIC, JOVAN
 ; APPLICANT: NAMRATH, MICHAEL
 ; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS FOR TREATING OR PREVENTING
 ; TITLE OF INVENTION: CANCER
 ; FILE REFERENCE: VOS-27
 ; CURRENT APPLICATION NUMBER: US/10/047,539
 ; CURRENT FILING DATE: 2002-01-15
 ; PRIOR APPLICATION NUMBER: EP 01 10 0914.9
 ; PRIOR FILING DATE: 2001-01-16
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 6
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
US-10-047-539-6
```

```
Query Match          34.7%; Score 25; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VPFVS 5
        |||||
Db       5 VPFVS 9
```

```
RESULT 70
US-10-073-300-1
 ; Sequence 1, Application US/10073300
 ; Publication No. US20030003535A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Reiter, Yoram
 ; TITLE OF INVENTION: SINGLE CHAIN CLASS I MAJOR HISTO- COMPATIBILITY COMPLEXES
 ; FILE REFERENCE: 02/23339
 ; CURRENT APPLICATION NUMBER: US/10/073,300
 ; CURRENT FILING DATE: 2002-06-25
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: synthetic peptide
US-10-073-300-1
```

```
Query Match          34.7%; Score 25; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VPFVS 5
        |||||
Db       5 VPFVS 9
```

```
RESULT 71
```

US-10-108-511-8
; Sequence 8, Application US/10108511
; Publication No. US20030017134A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Yoram
; APPLICANT: Avital, Lev
; TITLE OF INVENTION: METHODS AND PHARMACEUTICAL COMPOSITIONS FOR IMMUNE DECEPTION,
; FILE REFERENCE: PARTICULARLY USEFUL IN THE TREATMENT OF CANCER
; FILE REFERENCE: 01/23109
; CURRENT APPLICATION NUMBER: US/10/108,511
; CURRENT FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: HLA-A2-restricted synthetic peptide, derived from the melanoma d
; OTHER INFORMATION: fferentiation antigen gp100
US-10-108-511-8

Query Match 34.7%; Score 25; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPSV 5
Db 5 VPFSV 9

RESULT 72
US-10-080-013-4
; Sequence 4, Application US/10080013
; Publication No. US20030077246A1
; GENERAL INFORMATION:
; APPLICANT: Moriaty, Ann
; APPLICANT: Leturcq, Didier
; APPLICANT: Degraw, Juli
; APPLICANT: Heiskala, Maria
; APPLICANT: Peterson, Per
; APPLICANT: Jackson, Michael
; TITLE OF INVENTION: A CELL THERAPY METHOD FOR THE TREATMENT OF TUMORS
; FILE REFERENCE: CRT-1557
; CURRENT APPLICATION NUMBER: US/10/080,013
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-080-013-4

Query Match 34.7%; Score 25; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPSV 5
Db 5 VPFSV 9

RESULT 73
US-10-161-097-28
; Sequence 28, Application US/10161097
; Publication No. US20030096404A1
; GENERAL INFORMATION:
; APPLICANT: ROSENZWEIG, Michael
; APPLICANT: PYKETT, Mark J.
; APPLICANT: SCADDER, David T.
; APPLICANT: POZNANSKY, Mark C.
; TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION

TITLE OF INVENTION: FROM HEMATOPOIETIC PROGENITOR CELLS IN THREE-DIMENSIONAL
; FILE REFERENCE: C1005/7012/KA/ERG
; CURRENT APPLICATION NUMBER: US/10/161,097
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: US/09/574,749
; PRIOR FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: US 60/107,972
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: PCT/US99/26795
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 09/524,749
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Homo Sapiens source
US-10-161-097-28

Query Match 34.7%; Score 25; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPSV 5
Db 5 VPFSV 9

RESULT 74
US-10-224-286-30
; Sequence 30, Application US/10224286
; Publication No. US20030108517A1
; GENERAL INFORMATION:
; APPLICANT: Soo Hoo, William
; TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS
; COMPRISED GM-CSF AND METHODS OF MODULATING AN IMMUNE
; RESPONSE USING SAME
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESS: CAMPBELL & FLORES, LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/224,286
; FILING DATE: 19-Aug-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/902,516
; FILING DATE: 29-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IM 2442
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-10-224-286-30

Query Match 34.7%; Score 25; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSV 5
Db 5 VPFSV 9

RESULT 75
US-10-170-832-72
; Sequence 72, Application US/10170832
; Publication No. US2003010792A1
; GENERAL INFORMATION:
; APPLICANT: Chaux, Pascal
; APPLICANT: Vantomme, Valérie
; APPLICANT: Stroobant, Vincent
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Thielemans, Kris
; APPLICANT: Cortals, Jürgen
; TITLE OF INVENTION: MAG-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
; FILE REFERENCE: L0461/7052
; CURRENT APPLICATION NUMBER: US/10/170,832
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/166,448
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 72
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-170-832-72

Query Match 34.7%; Score 25; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSV 5
Db 5 VPFSV 9

RESULT 76
US-10-371-942-1
; Sequence 1, Application US/10371942
; Publication No. US20030223994A1
; GENERAL INFORMATION:
; APPLICANT: Hooogenboom, Henricus Renertus Jacobus Matthaeus
; APPLICANT: Reiter, Yoram
; TITLE OF INVENTION: MHC-PEPTIDE COMPLEX BINDING LIGANDS
; FILE REFERENCE: 10280-034001
; CURRENT APPLICATION NUMBER: US/10/371,942
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,994
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-371-942-1

Query Match 34.7%; Score 25; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSV 5
Db 5 VPFSV 9

RESULT 77
US-10-245-871-425
; Sequence 425, Application US/10245871
; Publication No. US2003023594A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: 11-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2013
; CURRENT APPLICATION NUMBER: US/10/245,871
; CURRENT FILING DATE: 2003-01-09
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 905
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 425
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-245-871-425

Query Match 34.7%; Score 25; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSV 5
Db 5 VPFSV 9

RESULT 78
US-10-465-811-73
; Sequence 73, Application US/10465811
; Publication No. US20040005338A1
; GENERAL INFORMATION:
; APPLICANT: BACHMANN, MARTIN F
; APPLICANT: RENNER, WOLFGANG A
; TITLE OF INVENTION: PACKAGED VIRUS-LIKE PARTICLES FOR USE AS ADJUVANTS:
; FILE REFERENCE: 1700.0290004
; CURRENT APPLICATION NUMBER: US/10/465,811
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 60/389,898
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 73
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-465-811-73

Query Match 34.7%; Score 25; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSV 5
Db 5 VPFSV 9

RESULT 79
US-10-168-417A-5
; Sequence 5, Application US/10168417A
; Publication No. US20040009185A1
; GENERAL INFORMATION:

```
/ APPLICANT: Emlage, Peter
/ APPLICANT: Barber, Brian
/ APPLICANT: Sambhara, Suryprakash
/ APPLICANT: Sia, Charles Dwo Yuan
/ TITLE OF INVENTION: Enhancing the Immune Response to an Antigen by Presensitizing with
/ FILE REFERENCE: 11014-18-US
/ CURRENT APPLICATION NUMBER: US/10/168,417A
/ CURRENT FILING DATE: 2002-11-15
/ PRIOR APPLICATION NUMBER: US 60/174,587
/ PRIOR FILING DATE: 2000-01-05
/ PRIOR APPLICATION NUMBER: PCT/CA01/00005
/ PRIOR FILING DATE: 2001-01-05
/ NUMBER OF SEQ ID NOS: 11
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 5
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide, amino acids 209-217 of gp 100, referred to as
/ US-10-168-417A-5
```

```
Query Match          34.7%; Score 25; DB 4; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 VPPSV 5
Db 5 VPPSV 9
```

```
RESULT 80
US-10-168-417A-7
/ Sequence 7, Application US/10168417A
/ Publication No. US2004009185A1
/ GENERAL INFORMATION:
/ APPLICANT: Emlage, Peter
/ APPLICANT: Barber, Brian
/ APPLICANT: Sambhara, Suryprakash
/ APPLICANT: Sia, Charles Dwo Yuan
/ TITLE OF INVENTION: Enhancing the Immune Response to an Antigen by Presensitizing with
/ FILE REFERENCE: 11014-18-US
/ CURRENT APPLICATION NUMBER: US/10/168,417A
/ CURRENT FILING DATE: 2002-11-15
/ PRIOR APPLICATION NUMBER: US 60/174,587
/ PRIOR FILING DATE: 2000-01-05
/ PRIOR APPLICATION NUMBER: PCT/CA01/00005
/ PRIOR FILING DATE: 2001-01-05
/ NUMBER OF SEQ ID NOS: 11
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 7
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide, amino acids 209-217 of modified gp 100, referred
/ US-10-168-417A-7
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Db 5 VPPSV 9
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